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OM nucleic - nucleic search, using sw model

Run on: August 16, 2002, 16:02:50 ; Search time 6647.57 Seconds
(without alignments)
11867.952 Million cell updates/sec

Title: US-09-787-657-3
3770
Sequence: 1 tactatagggcgccgcgaa.....aaaaaaaaaaaaaaaaaaaaa 3770

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank1:
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2: gb_hlg:*
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32: em_hlg_other:*
33: em_higo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Score Match Length DB ID Description

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2	3769.6	100.0	3770	6	AX099316	AX099316 Sequence
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4	3288.2	87.2	3464	9	HSAT272213	AJ272213 Homo sapi
5	3166.6	84.0	3213	6	AX098884	AX098884 Sequence
6	3166.6	84.0	3213	6	AX099304	AX099304 Sequence
7	3113.6	82.6	3114	6	AX098883	AX098883 Sequence
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13	1211.6	32.1	3209	6	AX099346	AX099346 Sequence
14	1197.4	31.8	3339	6	AX098927	AX098927 Sequence
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19	846.2	22.4	943	9	AB047621	AC104298 Homo sapi
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39	214	5.7	3186	6	AX098876	AX099296 Sequence
40	214	5.7	3186	6	AX099296	AX098877 Sequence
41	214	5.7	3248	6	AX098877	AX099297 Sequence
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ALIGNMENTS

RESULT 1
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DEFINITION Sequence 21 from Patent WO0119870.
ACCESSION AX098896
VERSION AX098896.1 GI:13538125
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 3770)
AUTHORS Brown,J.P. and Bertelli,F.
TITLE Secreted soluble $\alpha_2(\text{I})$ -2, $\alpha_2(\text{I})$ -3 or $\alpha_2(\text{I})$ -4
calcium channel subunit polypeptides and screening assays using
same
JOURNAL Patent: WO 0119870-A 21 22-MAR-2001;
FEATURES
source WARNER-LAMBERT COMPANY (US)
Location/Qualifiers
1..3770
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 1049 a 871 c 941 g 908 t 1 others

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Db	2281	CTGACAAGGGCGtTGAGGtTGCCTTCTCGGCACTCGcAGGGCCtTTCAGAAATCAACC	2340
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QY	3601	ttggcaagcatgcaaatgtgagttgtgcacatgatataacaccttcacacagaagaggac	3660
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LOCUS	AX099316	3770 bp	DNA linear PAT 02-APR-2001
DEFINITION	Sequence 21 from Patent WO0120336.		
ACCESSION	AX099316		
VERSION	AX099316.1	GI:13538471	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 3770)		
JOURNAL	Bertelli, F., Brown, J.P., Dissanayake, V., Suman-Chauhan, N. and		
FEATURES	Gee, N.S.		
source	Screening for alpha2delta-1 subunit binding ligands		
BASE COUNT	1049 a 871 c 941 g 908 t	1 others	
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Matches 3770; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
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Db	Accession	LOCUS	DEFINITION	ACCESSION	KEYWORDS	SOURCE	ORGANISM
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DEFINITION	Homo sapiens mRNA for calcium channel alpha2-delta3 subunit.						
ACCESSION	AJ272268						
VERSION	AJ272268.1						
KEYWORDS	calcium channel alpha2-delta3 subunit.						
SOURCE	human.						
ORGANISM	Homo sapiens						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
AUTHORS	1 (bases 1 to 3544)						
TITLE	Hanke, S., Bugert, P., Chudek, J. and Kovacs, G.						
JOURNAL	Cloning a calcium channel alpha2delta-3 subunit gene from a putative tumor suppressor gene region at chromosome 3p21.1 in conventional renal cell carcinoma						
MEDLINE	Gene 264 (1), 69-75 (2001)						
REFERENCE	2 (bases 1 to 3544)						
AUTHORS	Kovacs, G.						
TITLE	Direct Submission						
JOURNAL	Submitted (15-FEB-2000) Kovacs G., Department of Urology, University of Heidelberg, Laboratory of Molecular Oncology, Im Neuenheimer Feld 365, Heidelberg, 69120, GERMANY						
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ACCESSION	AX098884				
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ORGANISM	Homo sapiens				
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REFERENCE	1 (bases 1 to 3213)				
AUTHORS	Brown,J.P. and Bertelli,F.				
TITLE	Secreted soluble -g(a)2-g(d)-2, -g(a)2-g(d)-3 or -g(a)2-g(d)-4 calcium channel subunit polypeptides and screening assays using same				
JOURNAL	Patent: WO 0119870-A 9 22-MAR-2001;				
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OY	2784	aacaaattgctatacaatbtggctccctttaaaagaattacccttaactgactataccaagcctg	2843
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OY	2844	tgtagaccacaagaagaagcagcgaatggcgcccaatggcctctcgtatccctataatagcc	2903
Db	2701	TGTAGAGCCCAACAAAGAAAGCAGCATGTGGCGCCCTGCTGATTCCTGATTAATGCC	2760
OY	2904	ttccctctctgacgataaattgatatgataagacactgtgtctgttctcgttggtaatttaac	2963
Db	2761	TTTCTCTCTGCACTATAAATGATCATGACAGACTGTGTCTGTCTGTGGTAATTTTAAAC	2820
OY	2964	ctctgcaagltggttggcactccgataatgaacagctlaaagcccaagaatttgaacagacccgt	3023
Db	2821	CTTCTCAGTGTGGTGCACTCCGATATGACAGCTTAAGCCCAAGAATTTGAACAGACCCMG	2880
OY	3024	gagccttgtgatactggaataatccagcattcgtctcttgagcgacacatcaagagagactaca	3083
Db	2881	GAGCCTTGTGATATCAAGAAATATCCACATTTGCTCTGTGAGCGACCATCAAGAGAGCTACA	2940
OY	3084	gggaatatgtcgttgyaagactcgtcccaagtcctctgtgcatccagcnaatcccaagcagc	3143
Db	2941	GGGAATATTTGCTGTGAAAGACTGCTCCAAATCTTTGTTCATCCAGCAAAATCCCAAGCCAC	3000
OY	3144	aaacctgtcaatgltgtgtgtgagacagcagctgtcctctgtgaatcgtgtggcccccaatcac	3203
Db	3001	AACCTGTTCATGTGTGTGTGGTAGCAGACGCTCCTCTGTGAATCTGTGGCCCCCATCAAC	3060
OY	3204	atggcaccatgtgaataatcaaggtataataatcccttaagtgtgaaagtctaa-----	3256
Db	3061	ATGGCACCATTGGAATATGAGTATATATATATCCCTTAAGTGTGAACATCTTAAGGCCAG	3120
OY	3257	-----ggccagaagaatcagaagagggccccagaatcctgtcatggtcttcaatcct	3305
Db	3121	AAGATCCAGAAGGGCCCAAGAAGATCGAAAGGCCCCCAAGAAATCTTGTATATGCTTCCATCT	3180
OY	3306	gaggaagaatgcagaagagtgltggygggtgcgcg	3338
Db	3181	GAGGAGAAATGCAGAAGAGTGTGGGGGTGCGCG	3213

[illegible]

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Db 781 GTTAGACTTCAGTGGCAGCATGAAAGACTCCGTGTGACTATCGCGAAAGCAAGCTCTCA 840
QY 984 lccattctggaatacaactctgggaatgatactctctcaacataatgtctataatgaaag 1043
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Db 841 TCCATTTTGGATACACTTGGGGATGATGACTTCTCAACATAATTGCTTAAATGAGAGAG 900
QY 1044 ctccactatgttgaaaccttgccgtgaatgaaacttggltgcaagcgcaagacaacaaa 1103
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QY 1104 gaaacactcagaggaacatcctggaacaaactcttcgcaaaagaaattgaaagtgtgatata 1163
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Db 961 GAGCACTTCAGGGAGCATCTGGACAAACTTTTCGCCAAGGAATTTGAAATGTTGATATA 1020
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Db 2941 GGGAAATATTCCTGTGAAGACTGCTCCAAAGTCTTGTCTATCCGCAAAATCCCAAGAGC 3000
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Db 3121 AAGATCAGAAAGGCCGCAAGATCAGAAAGGCCGCAAGATCTGTGCTTCAATGCTTCT 3180
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Db 3181 GAGGAGATGCAAGGAGGTGTGGGGTGGCCG 3213

RESULT 7
AX098883 3114 bp DNA 1:near PAT 02-APR-2001
LOCUS AX098883
DEFINITION Sequence 8 from Patent WO0119870.
ACCESSION AX098883
VERSION AX098883.1 GI:13538119
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3114)
AUTHORS Brown,J.P. and Bell,J.F.
TITLE Secreted soluble -g(a)2,g(d)-2, -g(a)2,g(d)-3 or -g(a)2,g(d)-4
calcium channel subunit polypeptides and screening assays using
same
JOURNAL Patent: WO 0119870-A 8 22-MAR-2001;
WARNER-LAMBERT COMPANY (US)
FEATURES
source 1. 3114
Location/Qualifiers
BASE COUNT 868 a 704 c 789 g 752 t 1 others
ORIGIN
Query Match 82.6%; Score 3113.6; DB 6; Length 3114;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 444 aagaagtcgaagccgctcagcgcgtctgtagggctgcagaagaagcaccctgaacat 503
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Db 361 GAATTTGATGAGACTTACATGATGAATATCTCAATGCTGTGATGATGAATGAAGGAG 420
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Db 421 AAGACGGGAATTTTGGAGCTGGGAAGGAATTAATCACTTAAGCCCAAAAGACATTTT 480
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Db 481 AATATTTGCTGTGACATCATGCTTAAGTACCTCCAGTACCAAGACATGATACAC 540
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Db	1381	CTGACTGATGATCAAGGGCCCCCGTCTGATGACACACTGTAGCCATGCTGTGTTAGTAAg	1440
OY	1584	cagaacgaaacccagatcgaagggcatctctctggaagtggtctgagcagaatgtcccaatg	1643
Db	1441	CAGAAACGAAACCAATATGAAAGGGCATCTCTTGAGAGTGGTGGACAGATGTCCCACTG	1500
OY	1644	aaagaacctgcgaagaccatccccaatgcagaatctggagatccaaagttatgaccttga	1703
Db	1501	AAAGACTCTTGAAAGACCATCCCAATATACATTTAGGATATCAGGTTATGCTTTTCA	1560
OY	1704	atcccaaaataatgtrtaatacctgcagacatccggaaactcgaagctcgtctagcaagaagga	1763
Db	1561	ATCACAAATATAGTGTATATCTGAGACATCCGGAACCTCAGGCTGCTGTAGCAAGAGA	1620
OY	1764	aaaaagagaagaaacctaaactatagtagcgttgacacctctcgaagtvgagatvggaagac	1823
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OY	1824	cgagaatgaagctgcttgagaataatgcataatgcatacgaagaacgggaagttcttcataagag	1883
Db	1681	CGAGATGACGCTTGAGAAATGCTATGGTGTAATCGAAACACGGGAAGTTTCCATGTGAG	1740
OY	1884	gtgaaagaagacagtgcgaacaaagggaacgggtcttggtgatacacaatgaaactatata	1943
Db	1741	GTGAAAGAAGACAGTGACAAAGGAAACGGGTTTTGCTATGACAAATACACTACTATAT	1800
OY	1944	acagacatcaagggtaactccttcagattaggtgtgagccttcagaaagttcataggaat	2003
Db	1801	ACAGACATCAAGGCTACTCCTTTCACTTTTAGGTGTGCTGCGCTTTCCAGAGTCATGGGAA	1860
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Db	1861	TATTCTTCTCCAGCGGAATGTATACCATTCGAAGAAGCGCCTCATAGACTTATAGAACATCCGAT	1920
OY	2064	gtgtcccttggaagatgtagtgctctcctcgaacacagacctcacccctgagaaacggcat	2123
Db	1921	GTGTCTTGAGAGTATGATGATGCTCTACTGCAACACTGACCTTACACCTGTAGACCCGCAT	1980
OY	2124	ctgtctcaagttagaagaagatatgaagcttaactcaataaaggcaagaacactctgtccagagt	2183
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OY	2244	tattggaacccagctcgtgaccccaacaacatctgaaaatcttcgaagaagggcgtgaaagtgtcc	2303
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OY	2304	ttccctcggaactcgacagggcctctccagaatcaactgttgtccgggctgtagcagctc	2363
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OY	2424	ccctctcgtgtaacggaagagccgcttgagcagatctccagggagctctgcttaactgatacca	2483
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OY	2484	ctcgaacctggaacagtgcaataaagaacatgtgtgtgacagcaagtatacatccaagctc	2543
Db	2341	TTTCAGCACTGGACCAAGTCAATTAACCAATGTGTGTACAGCAAGTATCATCATCAGCTC	2400
OY	2544	ctggaatgaacggaatactcctcgtgtgtagcagcgtgtaggaattccagataaactgaaatt	2603
Db	2401	CTGGAATGAACGGAATCTCCTGTGTGTGCGCAGCTGTATAGCATTCAGATGAACCTTGAAATTT	2460
OY	2604	ttccaaaggaagttctggaactgcagcagacagatgtgtcttccctgtagtgcanaatgtctcc	2663

DB	2461	TTCCAAAGGAATTCCTGAGCTCCGACGACAGCTGTGCTTCCTCGATGCGAAATGCTCC	2520
QY	2664	atcagctgtgatagtgagactgttgactgttaacctcaataagacaataatgattcttctg	2723
Db	2521	ATCAGCTGTGATGATGAGAGACTGTGAAATGTTACCTCAATAGACAAATATGATTTATTTTGG	2580
QY	2724	gtgtctgaagactacacacagacttgagactcttctgtgagatcgagggagctgtgatg	2783
Db	2581	GTGTCTGAAGACTACACACAGACTGGAGACTTTTTTGGTGAATGAGAGGAGACTGTGATG	2640
QY	2784	aacaaatgtctaacaaatgggctcctttaaagaattacccttlatgactaccagaacatg	2843
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QY	2904	ttcctctctgcagtaaatgataatgatacagaactgttctgtgtccctgtgtgaattaac	2963
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QY	3144	aaactgttcatgtgtgtgtgtgacagacagctgctcctgtgaaatctgtgtggccccaacc	3203
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QY	3204	atggagcccatgtgaatcagagatataatgaatccctctaagtgtgaacggtctaaag	3257
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AX093303			
LOCUS	AX093303	3114 bp	DNA
DEFINITION	Sequence 8 from Patent WO0120336.		linear
ACCESSION	AX093303		
VERSION	AX093303.1	GI:13538465	
KEYWORDS			
ORGANISM	human.		
AUTHORS	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
	1 (bases 1 to 3114)		
	Bertelli,F., Brown,J.P., Dissenayake,V., Suman-Chaudhan,N. and		
	Gee,N.S.		
	Screening for alpha2delta-1 subunit binding ligands		
	Patent: WO 0120336-A 8 22-MAR-2001;		
	WARNER-LAMBERT COMPANY (US)		
FEATURES	Location/Qualifiers		
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BASE COUNT	868 a	704 c	789 g
ORIGIN		752 t	1 others

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Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 3114;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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ACCESSION	AX098882		
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Qy	1164	gctctgaaatgaagcccttcaaatctctgagtgtatcttaaccacaacgaggacaagaagatc	1223
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OY	1944	acagacatcaagggtlactcccttcagtttagtgctggcgcttccaaagttcatgggaa	2003
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REFERENCE	1 (bases 1 to 3710)		
AUTHORS	Klugbauer, N.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-SEP-1998) Klugbauer N., Institut fuer Pharmakologie und Toxikologie, Technische Universitaet Muenchen, Biedersteiner Str. 29, 80802, GERMANY		
REFERENCE	2 (bases 1 to 3710)		
AUTHORS	Klugbauer, N., Lacinova, L., Marais, E., Hobom, M. and Hofmann, F.		
TITLE	Molecular diversity of the calcium channel alpha2delta subunit		
JOURNAL	J. Neurosci. 19, 648-691 (1999)		
REFERENCE	Location/Qualifiers		
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AX098926 LOCUS AX098926 3209 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 51 from Patent WO0119870.
ACCESSION AX098926
VERSION AX098926.1 GI:13538143
KEYWORDS

SOURCE

human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3209)
AUTHORS Brown,J.P. and Bertelli,F.
TITLE Secreted soluble -g(a)2-g(d)-2, -g(a)2-g(d)-3 or -g(a)2-g(d)-4
calcium channel subunit polypeptides and screening assays using
same

JOURNAL JOURNAL Patent: WO 0119870-A 51 22-MAR-2001;

FEATURES WARNER-LAMBERT COMPANY (US)
LOCATION/Qualifiers

SOURCE

1..3209
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BASE COUNT 757 a 888 c 920 g 644 t
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163 AGATTCTCTGGAAAGAGTGAAGCTATGGCTGACACCTTGCGGGGAGCTGTATACA 222
310 tgcctgtaagctacccgcttccagctctgcgaagaatacagaagtagatagaag 369
223 CTGTGACCAATATCTAGGCTCTCTTGGTGCAGAAAGTAGACAGAGATGAGATCCA 282
370 acgttgcataagaaattgatacgctccaactggtcaagaagctggcaagaagctg 429
283 GTCTGAAGATCGAAGAGTGATGGATGGAGCTGTGAGAGAAATCTTCAGAGACATGG 342
430 aagagatgcttccaaagaagctcgaagcgctcgaagcgctcgtgtagagctgcagaaga 489
343 AGAATGATGCTGCGGAGGAAGTGCAGGGCGGTCCAGATCTGTGAGAGCTCCAGGAGG 402
490 gacacctgaaacatgaaattcgatgcagaactbaacgatgaattactcaatgctgctga 549
403 CCGACCTGAACCAAGAAATTAATGAAATCCCTGGTGTTCGACTATTAACACTCGGCTCGA 462
550 taaatgaagaaggacaagaagcggaatttttgagctgggaagaagattcaattagccc 609
463 TCAACGAGAGGAGAGAGAGGCACTTCGTGGAGCTGGGGCCGAGTTCCTCTGGAGT 522
610 caaatgaccaattbaataattgctctgtagaacatgctaaagtagagctccaagtaacca 669
523 CCAATGCTCACTTCAGACACCTGCGGTTGAACACTCCATCAGCAGGCTGAGCTGGCCA 582
670 ggaataatgcacaagaagaccctgcaattgcaatggggttattgctgaatcctctaa 729
583 CCAACGCTGACAAACAAAGACCAGATATTTAAATGAGAGCTACATCTCGAACCTTTGA 642
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790 gtcgaagaagccttcttaagcagatccggggaattaaatggaacacagatgagaatgag 849
703 GTCAACTGGAATCTTCAGATCTATCCAGATATTAATGAGACACGATGAGAAATGAG 762
850 tcatgtcctcgcagctgagaaacggaataatggtacatacccgagcaactctccgaag 909
763 TCAATTAATTTGATGCGCAACCGCGGTGTAATTAAGGATCACTTCTCCCAAG 822
910 acgtggtcattctagctgagcagctgagcaactgaaagacatccgtctactatcgga 969
823 ACATAGGATTTTGTGTAGAGTGAAGGCGCATGAGAGGGCTGAGATGACTATTTGCCA 882
970 agcaaaacagtcacatccatcttgatacaacttggggaatgaactcttcaacataatg 1029
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1090 acaggaacaacaagaagcacttcaaggagacatctggaacaactcttcgcaagaagattg 1149
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1150 gaattgtgataatagctcgaatggaagccttcaacatctgagtgatctcaaccacag 1209
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1183 ACGAGCGGTGTGAGAAATATACTGGCCAGACATCTAAAGGTCCGAGTTTTCATCTTACC 1242
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1564 ccaatgctgtgttagtaagcagaacgaacagatcgaaggacatcttctggagatg 1623
1483 CCATGCGAGTCTTCAAGCAAGAAAGCAAAAGCCATGCCATGCCATGCTCTCTGGGTGG 1542
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1861 agacggggaagtttccatggaagtgaagaagacagtcgaaaggggaacgagtttgg 1920
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1921 tgaatgaataatgactatatacagaacatcaaggatcactcttaagttagtggtag 1980
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1963 TGCATGACTTGTCTTCAACCCAGACCTTGCGCCCTGGCTGACTGATCTACTGCATCACAG 2022
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2023 ATATTGACCAAGACACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTCTCTCAACA 2082
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2221 tggtagtgcgcccaatgaaacglatatggaacagccttggccctcaacaaatctgaaatc 2280
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Db	2323	GCGTGTTCACCCCTGGACCGCTTC	CCCGCTGTGTGTACCCGACCGCTTCAGACATCTCTGCTG	2382
QY	2461	ggaagctctgctactcgatcccatcgaactgagccagca-----ataaagcaatg		2514
Db	2383	GCAGCTTCGTCTTCAACCTCCCGCTGGGACAGAAAGCACAGAAAGTGC	GGTGAACCCATGG	2442
QY	2515	tgtgtgacgcaagtacatccatccagctccctcggatggaacggaatctcctgtgtggcag		2574
Db	2443	TGTGTACGGCAAGCACACTGTGGGGGTGACCGTGTGACAAAGGAGACACCAATGCTGTGAG		2502
QY	2575	ctgtgaggaattcagaatgaactggaatttctccaaaggaagtctctggaactgcagcagac		2634
Db	2503	CCGGGGGGGCTCCAAATGAAGCTGGAATTCCTCCACCGCAAAATTTCTGAGGGCAACCGGGC		2562
QY	2635	agtgctctccctggaatgagcaaatgctccatcagctgtgatatga/aactggaattgt		2694
Db	2563	AGTGACAGCATGTGGATGTGGCGCGTGCACACAGAGCTGGAGGACAGTGATCTGGACTGCT		2622
QY	2655	aacctcatgacaataatgagattatcttggctgtgtcgtgaagactacaacagactggagact		2754
Db	2623	TGCTATCTGACAAACAAACGGGTTCATTCGATTCCTCAAGAGGCCGACAGAGCGGAAGAT		2682
QY	2755	tttttggggaagatcagaggagactgtgatagaaacaatttgtctaacaatlyggctcccttaaaa		2814
Db	2683	TTCTGGGGGAGGTGATGTGTGCTGTGTCGTGACCCACCTCTCAACGAWGSGGGTGTTCAGCC		2742
QY	2815	gaattacccttatgaccaccaagcaactgtgtagaagcaacaaggaagacagcagatggcg		2874
Db	2743	AAGTACACTATGTATATACATATACAGGCATGTGCAAACTTCGAGTGAACACCACTAGTCAG		2802
QY	2875	cccaatgcccctcctgatacctataatgctcctccctcctctgtcagtaaaatlygatalcagag		2934
Db	2803	CCCAACCCCTGGTACAGCCCAATTTCTGCTTCCTTGACGGCGACAGATGGGCTGTGCAAG		2862
QY	2935	aactgtctcttctcctgtgtgaaattaaacctctcgaagtgtgtggcaatccgatatgacag		2994
Db	2863	AGCTGTGCTCTTCTCTGCTGTGAGTGTGTGGGGTCCGTGATACGACAGGGGGCG		2922
QY	2995	-----ctaaagcccgaaattgaacagacagccctggagacct		3030
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QY	3031	gtgatactgaatatccagcaatcgtctcgtctgagcgacatcaaggajactacaggaata		3090
Db	2983	GGGACACGAGATACCCCGTGTGCGATGTGACAGCCGCCATCCGGGGAAGGCAACGGGATGG		3042
QY	3091	ttgtctgtgaaagactgctcccaagctccttgtcatccagcaaatccccaagcagcaacctgt		3150
Db	3043	TGGATGTGGGGGCCCTCCAGGAAGGATTTGTGTGTGTGCACAGATATCCCAACTACTATCC		3102
QY	3151	tcatgtgtgtgtgtgagacagctgtccctctgtgaaatctgtgtgcccccatcacatgagcac		3210
Db	3103	TCTCTCTGTGTGACAAACCCACCTGTGACTGTGACGACATCTTCCACACAGTGTGTGACAGAG		3162
QY	3211	ccattgaaatcaggtatataatgaatcccttaagtgtgaaag		3250
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RESULT 13				
LOCUS	AX099346	3209 bp	DNA	linear
DEFINITION	Sequence 51 from Patent WO0120336.			
ACCESSION	AX099346			
VERSION	AX099346.1	GI:13538489		
KEYWORDS				
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
	1 (bases 1 to 3209)			
	Bertelli,F., Brown,J.P., Dismanayake,V., Suman-Chauhan,N. and			
	Gee,N.S.			

TITLE	Screening for alphaDelta-1 subunit binding ligands
JOURNAL	Patent: WO 012036-A 51 22-MAR-2001;
FEATURES	WARNER-LAMBERT COMPANY (US)
source	location/Qualifiers 1..3209 /organism="Homo sapiens" /db_xref="taxon:9606"
BASE COUNT	757 a 888 c 920 g 644 t
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Query Match	32.1%; Score 1211.6; DB 6; Length 3209;
Best Local Similarity	63.6%; Pred. No. 3.7e-234;
Matches 1932; Conservative	0; Mismatches 1069; Indels 39; Gaps
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Oy	310 ttgctgtcaagtactccggtlccacagctcttcycaaaaagaatalacaagaatlgaaag 369
Db	223 CTGTGACCAAAATACTCAGGCTCTCTCTTCCTGCAGAAAGAATACAAGATGTGGATCCA 282
Oy	370 acgtttgccatagaagaatatgatygccctccaaactvglaaagaagcttgcgaagaatvg 429
Db	283 GTCTAAGATCAGAGAGGTGATGCGCTTCGACACTGCTGAGAAAGTTCTCAGAGGACATG 342
Oy	430 aagagatgtttcacagaagctctggagccgttaagcgttcttgttgaaggctgaagaag 489
Db	343 AGAATATCGCTGGGAGGAAAGTGCAGGCCGTCCAGATGTGGTGAAGCTGCCAGAGAG 402
Oy	490 cacaccgtgaacatgaatttgaatgcagaactacagtatgatatactlcaatgtctgtcta 549
Db	403 CGGACCTGAACCCAGATTCATGATTCCTCGTGTGTGACATTAACAACCTGGTCTCTA 462
Oy	550 taaatgaaagggaacaaagacgggaatttttggagcttgggaaagaaatcatccttagccc 609
Db	463 TCMAAGAGAGGAGCAGAAAGGCGCAACTTCGTGGAGCTGGCGCCCGAGTTCCTCTGGAGT 522
Oy	610 caaatgacattttaataatttgcctgtgaaatcaatgaatcttaagtgaagcgaagaacca 669
Db	523 CCAATGCTCTACTTCAGCAACTTCGCGGTGAACACTCCATCGACACCGTGCGAGCTGCCA 582
Oy	670 cgaacatgtacacaaagaccctgtcaattgtcaatgaggtttatbtgtatgaatcctcaa 729
Db	583 CCAAGCTGTACACAAAAGCCCCAGATATTTTAAATGAGATCTACATGTCTGAAGCCTTCA 642
Oy	730 acaaaatttttgatataactttgacgctgacccatctcatatgycagtlacttbgyaa 789
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Oy	910 acgttgatcatttgaatltgacgtctcagtgcagatggaatgaaagactccgtctgactatcgca 969
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Qy 1270 atgataaatcttggcaaaatacaattggccagatcgaaagtctcgaatctcgaatca 1329
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Dh 1423 ACATGAGACAGCAAGCTCTCTGAGCTCGCAGGCTGAGAGCTGAGACGCTGTCACACTGTGG 1482
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Dh 1723 TGTCCGAAGTGGAGTGGGAAGACCAGGCTGAATCTGTGAAGAACGCAATGATAGGG 1782
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Dh 1783 AAACAGGTACTCTCTGATGATGTGAAGTTCGATGATGAAGGAAGCGAGTTCTT 1842
Qy 1921 tgaatgaaatgactactataatacaagacatacaaggtactcctcttaagtttagtgag 1980
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Dh 2023 AATATTACCCAGACACCGGAAGCTCAGCAAGCTAGAGGCAATGATCCGCTTCTCCACCA 2082
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QY	2041	tgcaagacttaga	atcccca	tg	tgac	ctctggaaga	tgaa	tgctctctcgaacacty	2100
Db	1963	ttccattgacttgc	ttaccacca	acttgccctt	ggccgctt	gacttgat	ttcgtat	ctacag	2022
QY	2101	acctaac	cccttgagac	ccgcacat	ctgtctc	agttaga	agatlaa	gctlaac	2160
Db	2023	aatattgacc	ccagacac	ccggaagctc	agccagctg	agagccat	gatgcc	tttccat	2082
QY	2161	ggaaga	aacccctc	gtctccag	gtgata	agaat	tgatacca	agaagcccttttga	2222
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QY	2221	tggtgag	tgcccccatt	gaaagc	gat	tgagacsa	gcagctg	gcccacaa	2280
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QY	2281	ctgga	aagyg	cg	lyg	aggt	tg	ctctctc	2340
Db	2203	ctgaac	acagctg	gtgag	ac	atggccct	ttcttg	ggacac	2262
QY	2341	tggttctg	ggagctg	agagctca	acaatag	-----	-----	-----	2372
Db	2263	ttgttctg	gggctcc	gagaa	gagctt	ccagat	ggccctc	cttga	2322
QY	2374	-----	-----	acttc	gaaagct	tg	gcagaa	gagaa	2411
Db	2323	ttccgagaa	ggtctcc	gcagagaa	gattc	cttac	cttgagag	acagcc	2382
QY	2412	gcaag	acat	ctccctc	ctg	tacagga	agccgc	gtgag	2471
Db	2383	ctggac	cccttcc	ccgctt	gtg	tacccg	ccacg	cttca	2442
QY	2472	tactc	galtcc	catcc	aaagca	act	tgagca	gta	2525
Db	2443	tttcaac	ctccgct	ggagc	gaa	gagcc	gaa	gagtg	2502
QY	2526	agta	atccat	ccagct	ccctc	gtg	atga	acg	2585
Db	2503	agcaac	agctgtg	ggcgg	gtg	accctt	gcacaa	agac	2562
QY	2586	caga	tga	aaact	tgaa	ctt	tc	caa	2645
Db	2563	caaat	gaac	ctg	gga	attc	ctt	cc	2622
QY	2646	ctgga	t	g	caaa	tg	ctccat	agc	2705
Db	2623	gtgga	tggg	ccg	ctc	acac	agag	ctg	2682
QY	2706	aata	tga	at	t	at	ct	tg	2765
Db	2683	aacaa	cg	g	gtt	cat	ctt	g	2742
QY	2766	atc	ga	g	g	ag	ct	g	2835
Db	2743	gtgga	t	g	gt	ct	g	ct	2802
QY	2826	cat	ga	ct	aa	cc	at	g	2885
Db	2803	tatga	ct	at	ct	g	ct	g	2862
QY	2886	ctgga	ct	ct	ta	at	tg	ct	2945
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Db	2923	tttct	gt	g	at	ta	ct	g	2982

QY 2995 -----ctaagccccaagaattgaaacagaccctggagccttgytatactgaa 3041

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LOCUS	AX099347	3339 bp	DNA	linear	PAT 02-Apr-2001
DEFINITION	Sequence 52 from Patent WO0120336.				
ACCESSION	AX099347				
VERSION	AX099347.1	GI:13538490			
KEYWORDS	human.				
SOURCE	ORGANISM	Human.			
REFERENCE	AUTHORS	Geen,N.S.			
TITLE	JOURNAL	Screening for alpha2delta-1 subunit binding ligands			
FEATURES	source	1..3339			
BASE COUNT	ORIGIN	780 a 934 c 960 g 665 t			
Query Match	Best Local Similarity	31.88; Score 1197.4; DB 6; Length 3339;			
Matches 1993; Conservative	0; Mismatches 1096; Indels 88; Gaps 5;				
250	agataccgctcccgctggtgaagcctcgtgcgcctgcttggctgggagataaacc	309			
163	AGATTCTCTCGAAGAACATGAGCTATGCGGTGACACTTGGCGGGGACCTGTATACA	222			
310	ttgcgtctaagtaactccggtctccagcttcgtcaaaagaatataagaagatagagaag	369			
223	CTGTGACCAAAATPACTCAGCGCTCTCTCTGTCGCAAGAAATACAGAGATGTGAGTCCA	282			
370	acgttgcataagaagaattatgatggtcctccaactcgtgtataaagaactggcaagaatcgtg	429			
283	GTCGTGAAGATCGAGGAGCGTGGATGCGCTTGGAGCGTGGAGGAAGTCTCAAGAGACATGG	342			
430	aagaagatcttcacaagaagcctgaagccgctcagagcgctctctgttgaggagctcagaagaag	489			
343	AGAAATCTCTCGCGGAGGAAATCTCAGGCGGCTCCAGAAATCTGTGTGAAGCTCCAGAGAGG	402			
490	cacacctgaagaactttagatgcagactatacagtaatgaataactcaatgctgtgctga	549			
403	CCGACCTTGAAACCCAGATATCAATCAATCCCTGGTGTTCGACTATTACAACTGGTCTCGA	462			

OY	550	taatlgaagggacaaagacggygaatlcttttggagcttgggaagaaatcatcttaagccc	609
Db	463	TCAACGAGAGGGAGACGACAAAGGGCAACTCTTCGGAGCTGGGGCGCGGATCTCTGGAGT	522
OY	610	caatgagaccttaatttaatttgcctgtgaaacacagctcgaatgaatgacgtccaaatgaca	669
Db	523	CCAAATGCTCACTTACGACACCTGCGGTGACACCTTCATCAGCAAGCTGCAAGTCCCA	582
OY	670	cgaaatgtacaaanaagacccttgcgaatttgcatttggatttatttggctgaatctctaa	729
Db	583	CCAACGTTGACAAACAAAGACCCAGATATTTTAATGAGAGCTACATGCTGAAGCCTTGA	642
OY	730	acaaagtlltltgataaactttggaccggtgtaccatctctcattatgtgcagttacttggaa	789
Db	643	AMGCTGCTTCGTGGGAACACTCTCCAGAGAACCCAAAGTTTGACCTTGCAATATTTTGGCA	702
OY	790	gtgcaaaaggcttllttagcaglatccggggtatlaatltggagaccaga tggaaatggag	849
Db	703	GTGCACACTGGATTCTTTCAGATCATCTCCAGAGTAAATATGGAACCTGATGAGAAATGAG	762
OY	850	tcattgccttcgactgcaggaaccggaanaatgtgtacalccagcagcaactcttcgnaag	909
Db	763	TCATTAATCTTTTGAATGCCGGAACCGGGCTGGTACATTTGAAGCTGCTACTTCTCCAAAG	822
OY	910	acgtgtgcaattttagtttgaagtcagltgtgcagaa tggaaagacccgtctgaatctcgga	969
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OY	970	agcaaaagtlctcaalccactlltggatacactlttgggagtatgacttcttcaacataatgt	1021
Db	883	AGCACACCATCACCACCATCTTGGACACCTGGGGGAGATGACTCTGTAAATATCATAG	942
OY	1030	cttataatggggagcttccactatgttgaacacctgtcgtgaatgtgaactttgtgtcaagcg	1081
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OY	1090	acagagacaaanaagagcactltcagggagcatcttgacaaacttctgcgaagaatgt	1145
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OY	1150	gaatgttggatatagtctctgaatgaaggccttcaacatcttgaatgtatltcaaccacaegg	1205
Db	1063	GGGTGCTGGACCAAGCCCTTAGAGAAAGCCCTTCAGATCTGTGAAGCAAGTTCCAAGGGCCA	1122
OY	1210	gacaagaagatcatctgtcagtcagagcccaatgtctcaactaactgaatggsgtgcgaacct	1265
Db	1123	AGCAAGAGAACGCTCTGCAACCAAGGCCATCATGCTCATCAGCAAGAGGCTGCCGTGGAGACT	1187
OY	1270	atgatacaatcttgcacaanaataaatgtgcagatcgaatcgaagtltgcatalctcaataac	1325
Db	1183	ACGAGCGGTGTTGGAAGAAATATTAACGTGCGCAACATGTAAGGTCGCAAGTTTTCACATTAC	1247
OY	1330	tcatttgaagagagagcggtgttggcagacaatcctaagtgatgtgagccttgtgcacaaga	1385
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OY	1390	gatttlltaccagatctccaacttggctgtatgttgaaggagaatgtcactgaataactctc	1445
Db	1303	GCTACTACAGCAGATCTCAACGGTGGCGGACACCCAGAGAAAGCTGATGGAATACGTCC	1365
OY	1450	acgtgtcttagccggcccaaaatgcatacgaccagagacatgtatgtgtcgtggaccgaagctt	1505
Db	1363	ACGAGCTCAGCGCCCATGATGTCATCAACACACACACGACATCACTCTTGGACAGAGGCTT	1422
OY	1510	acatttgcagacacct-----gactgtatgtcaagggcccgctcgtatgtgacacattgtg	1565
Db	1423	ACATGAGACAGCAAGCTCTCAGCTCGAGGCTCAAGAGCTCGACACATCTCTCACCACTGTGG	1487
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Db	1483	CCATGACAGTCTTACGCAAGAAAGCAAAACGGATGCCATGTCATCTCTGGGTGGTGG	1544

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QY	1684	ctcaaggtatgacctttgcaatacaaatatgtratatctctgcagatcccgaaacca	1743
Db	1603	tgcacggatgaccttttctaaacaccacatgctgacttcttccattccgaccttc	1662
QY	1744	ggtctgcttgaagaaagaaaaagcgaa--ggaacctactatagtcgttgaac	1800
Db	1663	ggccctctctacagagagggagaaactaaacccaaacttaactaacaagctgagtc	1722
QY	1801	tctctgagtgagtgaggaaaccgagatgacgtgtgtgaaatgctatgylgaatcgaa	1860
Db	1723	tctccgaagtgtgagtgaggaaaccagctctaaactctggaacacccatgattcattatagg	1782
QY	1861	agaaggggaagtttccatiggaagtgaagaagacagtggaacaagggaaacgggtttgg	1920
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QY	1921	tgatgaacaatgactactatcatacagacaatcaaggtatctcttcaagtttagtggtg	1980
Db	1843	tctctgaccaaagatctacttcttcacgacatcagcacacccctttagctttgggggtgg	1902
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Db	1903	tgtgtctccggggccgacgagaaatcattcttctggggaaacgctgtggaagagcc	1962
QY	2041	tgcattgacttgaacatcccgatgtgtctcttgcgcagatgaatggtccctacgtgaacctg	2100
Db	1963	tgcattgacttcttccacccagacctggccctggcgcgtacgaggttactgcatacagag	2022
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Db	2023	attattgaccctgaacaccggaaactcagccagctacagaccctatgattccgcttctcacc	2082
QY	2161	gcaagaacacctgtctccagtgatgataaagaattgacccaagaagtlccttlttgacgcyg	2220
Db	2083	ggaagagaccagacctgagattgtagcagagagctgtgtccggagggctgtttgacggcg	2142
QY	2221	tgtgtgattgcccccatctgaagcgtatlttgacacagcctgagcctcaacaattctgaatat	2280
Db	2143	tgtgtgacgcccctcattgaaagccttactgacacagcctggccctcaaatgtgtccgagagt	2202
QY	2281	ctgacaaggggtgaggagttgacctctctctgcgaactgcagcgggcctctccagaataaac	2340
Db	2203	ctgaacacgctgtgtgacatgaccttctcttgggcacccgggcttgaccttctggaagacct	2262
QY	2341	tgattgtcggggctgagcagctcaccaatbaag-----	2373
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QY	2374	-----actctgaaagctgfcgacaagagagaacatttttaac	2411
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QY	2412	gaaagacatttccctctcgtgtaacgaagaagccgcgtgagacagatccagaggagcttgc	2471
Db	2383	ctggacgcgttcccgctgtgtgacccgacagccttcagacacattctgctggcagcttgcctc	2442
QY	2472	lactcgaatcccatcagcactgagcacagta-----atlaaagaatgltgltgacagca	2525
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QY	2526	agtaacatccatccagctcctgtagtaacggaatctcctgtgtgtgcaagctgttagcaat	2585
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Search completed: August 16, 2002, 20:10:20
Job time: 14850 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 16, 2002, 17:02:20 ; Search time 547.54 Seconds
(without alignments)
11821.343 Million cell updates/sec

Title: US-09-787-657-3

Perfect score: 3770
Sequence: 1 tactataggggcgccgcgaa.....aaaaaaaaaaaaaaaaaaaa 3770

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3769.6	100.0	3770	21	AA09253	Human alpha-2-delt
2	3769.6	100.0	3770	22	AA501414	Human secreted sol
3	3769.6	100.0	3770	21	AA057551	Human calcium chan
4	3399.2	90.2	3598	22	AA09261	Human alpha-2-delt
5	3166.6	84.0	3213	22	AA501409	Human secreted sol
6	3166.6	84.0	3213	22	AA057546	Human calcium chan
7	3113.6	82.6	3114	22	AA501408	Human secreted sol
8	3113.6	82.6	3114	22	AA057545	Human calcium chan
9	3056.6	81.1	3057	22	AA501407	Human secreted sol

10	3056.6	81.1	3057	22	AA057544	Human calcium chan
11	1908.2	50.6	2008	21	AA09260	Human alpha-2-delt
12	1545	41.0	1774	21	AA251626	Human membrane cha
13	1268.2	33.6	3345	24	AA517582	DNA encoding novel
14	1268.2	33.6	5073	24	AA09254	Human alpha-2-delt
15	1265.6	33.6	3228	24	AA517581	DNA encoding novel
16	1211.6	32.1	3209	22	AA501432	Human secreted sol
17	1211.6	32.1	3209	22	AA057569	Human calcium chan
18	1197.4	31.8	3339	22	AA501433	Human secreted sol
19	1197.4	31.8	3339	22	AA057570	Human calcium chan
20	1155.8	30.7	5713	21	AA09278	Human alpha-2-delt
21	1139.6	30.2	3201	22	AA501431	Human secreted sol
22	1139.6	30.2	3201	22	AA057568	Human calcium chan
23	933	24.7	4135	24	AA022004	Human transporters
24	837.6	22.2	1036	21	AA09288	Probe for northern
25	755.6	20.0	859	22	AA194285	Human neuroblastom
26	660.2	17.5	881	22	AA194363	Human neuroblastom
27	596	15.8	1452	21	AA09279	Human alpha-2-delt
28	502.2	13.3	1194	22	AA099517	Human protein enco
29	423	11.2	783	23	AA574094	DNA encoding novel
30	390.4	10.4	516	21	AA09290	Partial rat alpha-
31	293.4	7.8	1050	22	AA501412	Human secreted sol
32	293.4	7.8	1050	22	AA501412	Human secreted sol
33	248.6	6.6	969	22	AA57549	Human calcium chan
34	248.6	6.6	969	22	AA501411	Human secreted sol
35	235.6	6.2	912	22	AA57548	Human calcium chan
36	235.6	6.2	912	22	AA501410	Human secreted sol
37	232.8	6.2	912	22	AA57547	Human calcium chan
38	214	5.7	3186	22	AA09292	Human secreted sol
39	214	5.7	3186	22	AA501404	Human secreted sol
40	214	5.7	3248	22	AA501405	Human secreted sol
41	214	5.7	3248	22	AA057542	Human calcium chan
42	214	5.7	3327	22	AA501406	Human secreted sol
43	214	5.7	3327	22	AA057543	Human calcium chan
44	214	5.7	5482	21	AA09255	Human alpha-2-delt
45	214	5.7	5482	22	AA501413	Human secreted sol

ALIGNMENTS

RESULT	1
AAA09253	
ID	AAA09253 standard; cDNA; 3770 BP.
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AC	AAA09253:
XX	
DT	10-AUG-2000 (first entry)
XX	
DE	Human alpha-2-delta-C gene.
XX	
KW	alpha-2-delta-C; calcium channel subunit; 3p21.1; gabapentin; cytostatic;
KW	anticonvulsant; antimigraine; antiparkinsonian; antidepressant; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	144..3401
FT	CDS
XX	/*tag= a
XX	
PN	WO200020450-A2.
XX	
PD	13-APR-2000.
XX	
PF	07-OCT-1999; 99WO-US23519.
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PR	07-OCT-1998; 98US-0103322.
PR	30-OCT-1998; 98US-0106473.
PR	29-DEC-1998; 98US-0114088.
XX	
PA	(WARN) WARNER LAMBERT CO.
XX	
PI	Johns MA, Molodover B, Oford JD;

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Dh	2881	gctcctctgataccttataatgtccttccctctctgcagtaaaatgtgatacgaagaactg	2940
QY	2941	tctgttccctgggtggaatttaactctctgcagttgtgtgcatctccgatatgacaactaaag	3000
Dh	2941	tctgttccctgggtggaatttaactctctgcagttgtgtgcatctccgatatgacaactaaag	3000
QY	3001	ccaagaattgaacaacagaccccttgagccttgatatacgaatataccagatctgctctg	3060
Dh	3001	ccaagaattgaacaacagaccccttgagccttgatatacgaatataccagatctgctctg	3060
QY	3061	agcgacacatcaaggaagactacagggaaatattgtcttggaaagactgtccaagctcttg	3120
Dh	3061	agcgacacatcaaggaagactacagggaaatattgtcttggaaagactgtccaagctcttg	3120

OY	3121	tcattccagcaaatccccaagagaagaacctgtctcatatgtgtgtgtgtgagaaagcagcgtgcctct	3180
Db	3121	tcattccagcaaaaatccccaagagaagaacctgtctcatatgtgtgtgtgtgagaaagcagcgtgcctct	3180
OY	3181	gtgaatctgttggcccccatcaccatgagcaccacatctgaatcaggtatataatgaatccctta	3240
Db	3181	gtgaatctgttggcccccatcaccatgagcaccacatctgaatcaggtatataatgaatccctta	3240
OY	3241	agtggtgaacggtctaaagggccagagaatcagaaggcgccagaatctctgtcatatgtgccttc	3300
Db	3241	agtggtgaacggtctctaaagggccagagaatcagaaggcgccagaatctctgtcatatgtgccttc	3300
OY	3301	atccctgaggagaaatgcgaaggagtggtgggggtgcgcgagatctctcaagcccaagcagatcc	3360
Db	3301	atccctgaggagaaatgcgaaggagtggtgggggtgcgcgagatctctcaagcccaagcagatcc	3360
OY	3361	tccctctgcctccctctgcgttttgtatgctctctctcaagggtgacacgtgacatgagatgtcttc	3420
Db	3361	tccctctgcctccctctgcgttttgtatgctctctctcaagggtgacacgtgacatgagatgtcttc	3420
OY	3421	ttaactgacctggaagtgtctctcttggcatctcaaatcatgataaactgtgaaccacaatat	3480
Db	3421	ttaactgacctggaagtgtctctcttggcatctcaaatcatgataaactgtgaaccacaatat	3480
OY	3481	gggtgcacacatacagagacatgaatatatgccacaatcagacatcctcatcatattcttaac	3540
Db	3481	gggtgcacacatacagagacatgaatatatgccacaatcagacatcctcatcatattcttaac	3540
OY	3541	tgttgcgttgatatataactctctaaagatatgttgcacaaagttatctatcatcttcttact	3600
Db	3541	tgttgcgttgatatataactctctaaagatatgttgcacaaagttatctatcatcttcttact	3600
OY	3601	tgcgcagtcacatgcacaaatgttgagtttgcacacatgaatacaccctctcatcagaatctggac	3660
Db	3601	tgcgcagtcacatgcacaaatgttgagtttgcacacatgaatacaccctctcatcagaatctggac	3660
OY	3661	cgcgaagtgtgtgaagcagtgctccctctgcgttgaaacctatcgaaaccaatttaaaactgtg	3720
Db	3661	cgcgaagtgtgtgaagcagtgctccctctgcgttgaaacctatcgaaaccaatttaaaactgtg	3720
OY	3721	tactctttaaataaagtatatataataatcatataaaaaaataaaaaaataaaaaa	3770
Db	3721	tactctttaaataaagtatatataataatcatataaaaaaataaaaaaataaaaaa	3770
RESULT 4			
AAAO9261			
ID	AAAO9261 standard; cDNA: 3598 BP.		
XX			
AC	AAAO9261;		
XX			
DT	10-AUG-2000 (first entry)		
XX			
DE	Human alpha-2-delta-C gene splice variant.		
XX			
KW	alpha-2-delta-C; calcium channel subunit; 3p21.1; gabapentin; cyostatic;		
KW	anticonvulsant; antitrigemine; antiparkinsonian; antidepressant;		
KW	splice variant; ss.		
XX			
OS	Homo sapiens.		
XX			
OS	WO200020450-AZ.		
XX			
PN	13-APR-2000.		
PD			
XX			
PE	07-OCT-1999; 99WO-US23519.		
XX			
PR	07-OCT-1998; 98US-0103322.		
XX			
PR	30-OCT-1998; 98US-0106473.		
XX			
PR	29-DEC-1998; 98US-0114088.		
XX			
PA	(WARN) WARNER LAMBERT CO.		
XX			

PI Johns MA, Moldover B, Offord JD:
XX
XX WPI; 2000-303744/26.
XX
XX New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
PT proteins, useful in the treatment of epilepsy, migraine, chronic pain,
PT anxiety, multiple sclerosis or cancer
XX
XX
XX Claim 22; Page 85-86; 86pp: English.
XX
XX The alpha-2-delta-C gene encodes a calcium channel subunit polypeptide.
CC The gene has been mapped to chromosome 3p21.1. This gene and the related
CC alpha-2-delta-D and -B genes are useful for protecting mammalian cells
CC from abnormal calcium flux by introducing expression vectors containing
CC the respective gene into mammalian cells. The antisense genes are also
CC useful for treating or preventing epilepsy. The alpha-delta-2-A protein
CC is a high-affinity binding target of the anti-consefent drug gabapentin.
CC Therefore, alpha-delta-2 proteins may also be targeted to treat
CC seizure-related syndromes, migraine, ataxia, vestibular defects, chronic
CC pain, sleep interference, anxiety, amyotrophic lateral sclerosis (ALS),
CC multiple sclerosis, mania, tremor, parkinsonism, substance abuse or
CC addiction syndromes, mood, depression or cancer.
XX
XX Sequence 3598 BP; 1004 A; 836 C; 904 G; 853 T; 1 other;
SQ

[illegible]

OY	661	aagtaaccaagaaacatgtaacaaagaacccgccaattgtcaatgggtttatgtgtctg	720
Db	661	aagtaaccaagaaacatgtaacaaagaacccgccaattgtcaatgggtttatgtgtctg	720
OY	721	aattctcaacaagaagttttgtatgaataactttgacccgttgaccatctcttcatactggagct	780
Db	721	aattctcaacaagaagttttgtatgaataactttgacccgttgaccatctcttcatactggagct	780
OY	781	actttggaaagtgcaaaagggtcttttttaaggcagatccggggatataaayggnaaccaagatg	840
Db	781	actttggaaagtgcaaaagggtcttttttaaggcagatccggggatataaayggnaaccaagatg	840
OY	841	agaaatgagatcatgtgcttctgtactgtcagaaacccgaaatggtataactcagcgagaactt	900
Db	841	agaaatgagatcatgtgcttctgtactgtcagaaacccgaaatggtataactcagcgagaactt	900
OY	901	ctccgaaagaacgltggtcatcttattgttgaagctcagtgacagatgaaaygactccgtctga	960
Db	901	ctccgaaagaacgltggtcatcttattgttgaagctcagtgacagatgaaaygactccgtctga	960
OY	961	ctatcgcgaagccaacacgcttcatacttattgtgatacacttgggagtgatgactcttca	1020
Db	961	ctatcgcgaagccaacacgcttcatacttattgtgatacacttgggagtgatgactcttca	1020
OY	1021	acataatgtgcttaataagaaagagctccactatgttgaaaccttgcctcgatgtgaactttgg	1080
Db	1021	acataatgtgcttaataagaaagagctccactatgttgaaaccttgcctcgatgtgaactttgg	1080
OY	1081	tgcgaagcgcgaacagacaacaaagaagcacttcaaggagcatctgtgacaaacttttcgcca	1140
Db	1081	tgcgaagcgcgaacagacaacaaagaagcacttcaaggagcatctgtgacaaacttttcgcca	1140
OY	1141	aaggaatcttgaaatgttgatataagctcttaataagagccctcaacctctcgagtgatttca	1200
Db	1141	aaggaatcttgaaatgttgatataagctcttaataagagccctcaacctctcgagtgatttca	1200
OY	1201	accacaacgagacaagagaaagatctgtcagatccagccatcatgtcataactgatatggcgcg	1260
Db	1201	accacaacgagacaagagaaagatctgtcagatccagccatcatgtcataactgatatggcgcg	1260
OY	1261	tgggacacctatgatacaactttctgcacaatacaattggcccaatgcgaagggttcgactct	1320
Db	1261	tgggacacctatgatacaactttctgcacaatacaattggcccaatgcgaagggttcgactct	1320
OY	1321	tcaataaccatcatgtagacgagagctgagcttttgcagaacatactaaagtgtgagtgcgtctg	1380
Db	1321	tcaataaccatcatgtagacgagagctgagcttttgcagaacatactaaagtgtgagtgcgtctg	1380
OY	1381	ccaaacaaaggatttttttaaccagatctccaacttggctgtagtgtgcagagagaatgtcatg	1440
Db	1381	ccaaacaaaggatttttttaaccagatctccaacttggctgtagtgtgcagagagaatgtcatg	1440
OY	1441	aataccctcaacgltgcttagagccggcccaaaagtcatcgaacacaggaagaatgtagtggttga	1500
Db	1441	aataccctcaacgltgcttagagccggcccaaaagtcatcgaacacaggaagaatgtagtggttga	1500
OY	1501	ccgaagacttaacatgtaacagacactctgacgtgatatcaaggcccggtcgtatgaccacatg	1560
Db	1501	ccgaagacttaacatgtaacagacactctgacgtgatatcaaggcccggtcgtatgaccacatg	1560
OY	1561	tagccaatgacctgtgttttagtaagcagaacagaaacccagatctcgaaagggtatcttctctggag	1620
Db	1561	tagccaatgacctgtgttttagtaagcagaacagaaacccagatctcgaaagggtatcttctctggag	1620
OY	1621	tgtgttgacagagatgtcccggtgaagaagaactcttcgaagaccatccccaatacaagttag	1680
Db	1621	tgtgttgacagagatgtcccggtgaagaagaactcttcgaagaccatccccaatacaagttag	1680
OY	1681	ggattcaacggtatgatgcttttgcaatccacaataatggtatatacctgtagcagcatccggaac	1740
Db	1681	ggattcaacggtatgatgcttttgcaatccacaataatggtatatacctgtagcagcatccggaac	1740

QY	1741	tcagctcgcgtctacgaaagagaaaaagcgcgaaggaacaccttactatctgttcgctttgac	1800
Db	1741	tcagagctgcgtctacgaaagagaaaaagcgaaggaacaccttactatctgttcgctttgac	1800
QY	1801	ctctcgcgaagtgcgaatgcggaaagaccgcgaatgcgtctgttcggaatgcctatgttgaaatcga	1860
Db	1801	ctctcgcgaagtgcgaatgcggaaagaccgcgaatgcgtctgttcggaatgcctatgttgaaatcga	1860
QY	1861	agacgcggagaaatttccatctgaaagtgcgaagaaagcaatgcgaaacaaaggaacgcggctttcgg	1920
Db	1861	agacgcggagaaatttccatctgaaagtgcgaagaaagcaatgcgaaacaaaggaacgcggctttcgg	1920
QY	1921	tgatgcgaacaaatgcactactattatatacagacaatcaaggtgactctcttcagcttgaatgtctcg	1980
Db	1921	tgatgcgaacaaatgcactactattatatacagacaatcaaggtgactctcttcagcttgaatgtctcg	1980
QY	1981	cgctttccgaagagctgcatacggaataattctctccgcgaaggaatgtaacacatcgaaagaagcc	2040
Db	1981	cgctttccgaagagctgcatacggaataattctctccgcgaaggaatgtaacacatcgaaagaagcc	2040
QY	2041	tgcatgactctgaaacatccccaatgcgtcttccttcgcaatgaaatgcgtccactatgcgaacatcg	2100
Db	2041	tgcatgactctgaaacatccccaatgcgtcttccttcgcaatgaaatgcgtccactatgcgaacatcg	2100
QY	2101	aactaacaccctgcagaccgcacatcgtctctcaatgtagaagcgaatgaagctctacactaaag	2160
Db	2101	aactaacaccctgcagaccgcacatcgtctctcaatgtagaagcgaatgaagctctacactaaag	2160
QY	2161	gcaaaagaaacctgcgtctccaaatgtgataaagaatgtatccaagaatgcctttttgacgcgg	2220
Db	2161	gcaaaagaaacctgcgtctccaaatgtgataaagaatgtatccaagaatgcctttttgacgcgg	2220
QY	2221	tggtgcgaatgcgcccatctgaaagcgtatattgcgaacgcgcgcgcctccaaacaaatctgaaat	2280
Db	2221	tggtgcgaatgcgcccatctgaaagcgtatattgcgaacgcgcgcgcctccaaacaaatctgaaat	2280
QY	2281	ctgcacaaggcgcgtgcgaaggtgtgcctctccctgcgcactgcgcgcgcgcctccacgaatcaacc	2340
Db	2281	ctgcacaaggcgcgtgcgaaggtgtgcctctccctgcgcactgcgcgcgcgcctccacgaatcaacc	2340
QY	2341	tggttgcgcgggcgtgcgaacgtctcaacaaatcagaactctctctgaaagctgcgcgaagaagga	2400
Db	2341	tggttgcgcgggcgtgcgaacgtctcaacaaatcagaactctctctgaaagctgcgcgaagaagga	2400
QY	2401	acatttttaaagcgcgaacattctccctctcctgcgcgaacgcgcgtgcgaacgaattccag	2460
Db	2401	acatttttaaagcgcgaacattctccctctcctgcgcgaacgcgcgtgcgaacgaattccag	2460
QY	2461	ggagcttcgtctactgcatacccatctcaagcactgcgaacagtcataaagaacatgtgcgga	2520
Db	2461	ggagcttcgtctactgcatacccatctcaagcactgcgaacagtcataaagaacatgtgcgga	2520
QY	2521	cagcaagtatacatccatccagctctctgcgaatgcgaacgtcttcgttcgcgaactgtag	2580
Db	2521	cagcaagtatacatccatccagctctctgcgaatgcgaacgtcttcgttcgcgaactgtag	2580
QY	2581	gcattcgcgaatgcgaactctgaaatttttccaaaggaagcttcgcgaactgcgcgaacgaagctgcg	2640
Db	2581	gcattcgcgaatgcgaactctgaaatttttccaaaggaagcttcgcgaactgcgcgaacgaagctgcg	2640
QY	2641	cttccctctgaaatgcgaacatgcatacagctgtgatgtatgcgaactgcgaatgttactccca	2700
Db	2641	cttccctctgaaatgcgaacatgcatacagctgtgatgtatgcgaactgcgaatgttactccca	2700
QY	2701	tagacaataatgcgaattatttttcggtgcgaagactacaacacagacgcgcgaactttttg	2760
Db	2680	-----agactgcgaactttttg	2697
QY	2761	gtgcgaatcgcgaagcgcgtgtatgcgaacaaatgtctaaacaaatgcgccttttaagaagaaat	2820
Db	2698	gtgcgaatcgcgaagcgcgtgtatgcgaacaaatgtctaaacaaatgcgccttttaagaagaaat	2757
QY	2821	ccctttatgcatacgaacgaactgtctagagccaacaaaggaagcgcgaatgcgcgcacgt	2880

[illegible][illegible]

OY	264	gtgtgtgaagctctcgggcctcggcttcttggctggggagataaaatccatctgctgcgaatgc	323
Db	121	gtgtgtgaagctctcgggcctcggcttcttggctggggagataaaatccatctgctgcgaatgc	180
OY	324	tcgggttcccgagctctcgcgaagaagaatacaaaaggtctggaagaagagtttgcgaatgaa	383
Db	181	tcgggttcccgagctctcgcgaagaagaatacaaaaggtctggaagaagagtttgcgaatgaa	240
OY	384	gaaattgatctgcctccaactcgtgtaaagaagcgtcgcaaaagaaacatctgaaagatcttccac	443
Db	241	gaaattgatctgcctccaactcgtgtaaagaagcgtcgcaaaagaaacatctgaaagatcttccac	300
OY	444	aagaagctctgaagcgtcagcgctctgtgtgagcgtctgcgaagaagacacactgaaaacat	503
Db	301	aagaagctctgaagcgtcagcgctctgtgtgagcgtctgcgaagaagacacactgaaaacat	360
OY	504	gaatttgatgcagacttacaagtataataattcctaagtctgtgtgatataatgaaaggagac	563
Db	361	gaatttgatgcagacttacaagtataataattcctaagtctgtgtgatataatgaaaggagac	420
OY	564	aaaagcggagatttttttggagcgtcggaagaagattcaattcttgcccccaatgagacattt	623
Db	421	aaaagcggagatttttttggagcgtcggaagaagattcaattcttgcccccaatgagacattt	480
OY	624	aataatttgcctctgaaacacatcagtcctaagtgcctccaagtacccaagaaatgctaacac	683
Db	481	aataatttgcctctgaaacacatcagtcctaagtgcctccaagtacccaagaaatgctaacac	540
OY	684	aaagaaccctgcaattgtcgaattgggtttatgtgtctgaattctctaacaaaagttttgta	743
Db	541	aaagaaccctgcaattgtcgaattgggtttatgtgtctgaattctctaacaaaagttttgta	600
OY	744	gataactctaacccgttaacccatctcccatatgacgaatttggaaagtgcgaagaagcttt	803
Db	601	gataactctaacccgttgcgcgcacatctcccatatgacgaatttggaaagtgcgaagaagcttt	660
OY	804	tttagcagatctccggggatctaaatgtggaaccaagatctgaagtcatctgtgccttcgac	863
Db	661	tttagcagatctccggggatctaaatgtggaaccaagatctgaagtcatctgtgccttcgac	720
OY	864	tcgacgagaccgaaaatgtatcatccagcagcaactctccgaaagacgctgtgcaattta	923
Db	721	tcgacgagaccgaaaatgtatcatccagcagcaactctccgaaagacgctgtgcaattta	780
OY	924	gtttacgctcagctgacgacatcgaaaggacccgtctgacatctcgagacgaacacgctcca	983
Db	781	gtttacgctcagctgacgacatcgaaaggacccgtctgacatctcgagacgaacacgctcca	840
OY	984	tccaattcttgatacaactctgggagatgatactgactcttccaacatatctgtctataatgagag	1043
Db	841	tccaattcttgatacaactctgggagatgatactgactcttccaacatatctgtctataatgagag	900
OY	1044	cttcaactatgtgaaacctgtgcctgaaatggaactttgtgtgcaagccgtaacgaaacaacaa	1103
Db	901	cttcaactatgtgaaacctgtgcctgaaatggaactttgtgtgcaagccgtaacgaaacaacaa	960
OY	1104	gagcaactctgaaggagacatctcggaacaacttcttcgccaagaagatctgtaatttggatata	1163
Db	961	gagcaactctgaaggagacatctcggaacaacttcttcgccaagaagatctgtaatttggatata	1020
OY	1164	gctctgataatagagccttcaacatctctgagtgattccaacacacggtgacaaggaagtatac	1223
Db	1021	gctctgataatagagccttcaacatctctgagtgattccaacacacggtgacaaggaagtatac	1080
OY	1224	tgcsagtcaggcacatcgtctacataactgtatggggcgtgtgagacacctatgatataactctt	1283
Db	1081	tgcsagtcaggcacatcgtctacataactgtatggggcgtgtgagacacctatgatataactctt	1140
OY	1284	gcaaaatatacaatttggccaagtctgaaaggtctgcattcttcaactacacttgagcagag	1343
Db	1141	gcaaaatatacaatttggccaagtctgaaaggtctgcattcttcaactacacttgagcagag	1200

QY	1344	gctgcgcttgcagacaaactctaaaytgbatggtccgtgcgtgcacaaagattttttaccag	1403
Db	1201	gctgcgcttgcagacaaactctaaatgbatggtccgtgcgtgcacaaagattttttaccag	1260
QY	1404	atctccaccttgcgcgtatgctgcagagaaatgctaatgtatactctcaacgttccttagccg	1463
Db	1261	atctccaccttgcgcgtatgctgcagagaaatgctaatgtatactctcaacgttccttagccg	1320
QY	1464	cccaaatgcatcgcagacgaagacatgatatggtgtgtgcacgaagcttcaatgtacagacat	1523
Db	1321	cccaaatgcatcgcagacgaagacatgatatggtgtgtgcacgaagcttcaatgtacagacat	1380
QY	1524	ctgactgtatgatacgaagcccgctccctgtatgtacacactgtacacatgctgtgttaataag	1583
Db	1381	ctgactgtatgatacgaagcccgctccctgtatgtacacactgtacacatgctgtgttaataag	1440
QY	1584	cagaaacgaaacocagatcgaagaaggaattctttcttggaagtggtgtgcacaaagtgtcccaagt	1643
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QY	1644	aaagaactcttgaacacccatccccaatacagaatgaagatctcaggcttaatgctcttgca	1703
Db	1501	aaagaactcttgaacacccatccccaatacagaatgaagatctcaggcttaatgctcttgca	1560
QY	1704	atcacaaataabgtgtatatactctgcagcatcccggaactcaagctgtctgacgaagaagga	1763
Db	1561	atcacaaataabgtgtatatactctgcagcatcccggaactcaagctgtctgacgaagaagga	1620
QY	1764	aaaaagcgaaggaagaaacctaatatagtagcgtttgacctctcttggtgtgtgagtggaagac	1823
Db	1621	aaaaagcgaaggaagaaacctaatatagtagcgtttgacctctcttggtgtgtgagtggaagac	1680
QY	1824	cgaagatgcgctgttgagaagaatgctatggtgtgatcgaagaacgggaagtttccatgag	1883
Db	1681	cgaagatgcgctgttgagaagaatgctatggtgtgatcgaagaacgggaagtttccatgag	1740
QY	1884	gtcaagaagacacgttgacaagaaggggaaacgggttttgtgtatgacaaatgtaactatlat	1943
Db	1741	gtcaagaagacacgttgacaagaaggggttttgtgtatgacaaatgtaactatlat	1800
QY	1944	acagacatcaaggggtattccctttcaagtttaagtggtgcgctttccagaaggtcatagggaaa	2003
Db	1801	acagacatcaaggggtattccctttcaagtttaagtggtgcgctttccagaaggtcatagggaaa	1860
QY	2004	tattcttcgcgaaggaatgatacactgcaagaagggccgtgcatagtactagaacatcccgat	2063
Db	1861	tattcttcgcgaaggaatgatacactgcaagaagggccgtgcatagtactagaacatcccgat	1920
QY	2064	gtctcccttgcgcagatgaaatggttccctactgtcacaacatgtacaccccttgagcacccgat	2123
Db	1921	gtctcccttgcgcagatgaaatggttccctactgtcacaacatgtacaccccttgagcacccgat	1980
QY	2124	ctgtctcagtttagaagcgaattaaagctactactaaaggaagcaactctgtctccagtg	2183
Db	1981	ctgtctcagtttagaagcgaattaaagctactactaaaggaagcaactctgtctccagtg	2040
QY	2184	gataaagaatgatccacaagaagtgctcttttgaacgggtgtgtgagtgcccccatgtgaagcg	2243
Db	2041	gataaagaatgatccacaagaagtgctctcttttgaacgggtgtgtgagtgcccccatgtgaagcg	2100
QY	2244	tatttgaccagccttgcgacctcaacaacatctgaaaaattctgacaagggcgttgaaggttgc	2303
Db	2101	tatttgaccagccttgcgacctcaacaacatctgaaaaattctgacaagggcgttgaaggttgc	2160
QY	2304	tctctccggaactcgcagcgggctctccagaatcaacctgtttgtcggggtcgtgaacgctc	2363
Db	2161	tctctccggaactcgcagcgggctctccagaatcaacctgtttgtcggggtcgtgaacgctc	2220
QY	2364	accaaactaggaattctcctaaagctgtgcgaacaaggaacatttttaacgcagacatttc	2423
Db	2221	accaaactaggaattctcctaaagctgtgcgaacaaggaacatttttaacgcagacatttc	2280
QY	2424	cctctctgtacacgaagcgcgctgtgaagagatctccagaagacgttcgtctactatgcatcca	2483

QY 504 gaatttgatgcagactacagatagaaatctcatgtctgtcgtatgaataatgaaaggagc 563
|||||
Db 361 gaatttgatgcagactacagatagaaatctcatgtctgtcgtatgaataatgaaaggagc 420
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Db 3181 gaggagaatgtcaagggaggt 3213

RESULT 7
AAS01408
ID AAS01408 standard; cDNA: 3114 BP.
XX
AC AAS01408;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human secreted soluble alpha2delta calcium channel subunit #5 cDNA.
XX
KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW filter binding assay; wheat germ lectin flashplate assay; ss.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT CDS 1..3114
FT /tag- a
FT /partial
FT /product= "Alpha2delta calcium channel subunit #5"
FT /note= "This sequence lacks a stop codon"
XX
PN WO200119870-A2.
XX

PD 22-MAR-2001.
XX
XX 18-SEP-2000; 2000MO-EP09137.
XX
XX 16-SEP-1999; 99US-0397550.
XX
XX (WARN) WARNER LAMBERT CO.
XX
XX Brown JP, Bertelli F;
XX
XX WPI: 2001-235262/24.
XX P-PSDB: AAU01018.
XX
XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or
PT Wheat Germ Lectin Flashplate assays -
XX
XX
PS Claim 39; Page 70-71; 160pp; English.
XX
XX The present sequence encodes for human secreted calcium channel
CC alpha2delta subunit #5 which is soluble and retains the functional
CC characteristics of the full length or wild type alpha2delta subunit
CC (AAU01025) from which it is derived. The invention relates to truncated
CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
CC which retain their affinity for radioactively labeled gabapentin. The
CC voltage-dependent calcium channel (VDCC) complexes present in neuronal
CC and non-neuronal tissues including heart and skeletal muscle. Numerous
CC soluble forms of the human calcium channel alpha2delta subunits
CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the
CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are
CC described. The secreted soluble alpha2delta subunit may be used in assays
CC e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,
CC filter binding or wheat germ lectin flashplate assays to detect or
CC measure the binding or interaction of a ligand (e.g. gabapentin,
CC L-Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine,
CC L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel
CC alpha2delta subunit.
CC
XX
SO Sequence 3114 BP; 868 A; 704 C; 789 G; 752 T; 1 other;

Query Match 82.6%; Score 3113.6; DB 22; Length 3114;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 atggcggggcgccggcgccggcgccggcgccggcgccggcgccggcgccggcgccggcgccggcgcc 60
Qy 204 ggcctctctcagcgccggcgccggcgccggcgccggcgccggcgccggcgccggcgccggcgccggcgcc 263
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Oy	2784	aacaacattgcatcaaacacacagggcctcccttbaaagaatatcaacctltaatgatcatcaacagccatg	2843
Dd	2641	aacaacattgcatcaacacatgggcctcccttbaaagaataatcaacctltaatgatcatcaacagccatg	2700
Oy	2844	tgttagagccaacagaagaaaacagcagatgycgcgccatgccccctcccttgatccctataatgac	2903
Oy	2904	ttccctctctgcgaagaaatctgatalcalcatgacagaaattgctctgttccctgtgtgaatttac	2963
Dd	2761	ttccctctctgcgaagaaatctgatalcalcatgacagaaattgctctgttccctgtgtgaatttac	2820
Oy	2964	ctctgcagcttggtggtgcuccccgatgatgacagcgtcaaaagcccagaatctgaacaagaccctg	3023
Dd	2821	ctctgcagcttggtggtgcuccccgatgatgacagcgtcaaaagcccagaatctgaacaagaccctg	2880
Oy	3024	gagccctgtgtgaatctgaatctccagaattcgtctcgaagcagacatcaagaagagatcata	3083
Dd	2881	gagccctgtgtgaatctgaatctccagaattcgtctcgaagcagacatcaagaagagatcata	2940
Oy	3084	gggaalatlgtcttgatgaagcgtctccaaagtcccttgtatccatcagaacaaatcccagaagcagc	3143
Dd	2941	gggaalatlgtcttgatgaagcgtctccaaagtcccttgtatccatcagaacaaatcccagaagcagc	3000
Oy	3144	aacctgttcatgtgtgtgtgtgtgagcagcagctgcctctgtgaattctgtgtgcccccatcac	3203
Dd	3001	aacctgttcatgtgtgtgtgtgtgagcagcagctgcctctgtgaattctgtgtgcccccatcac	3060
Oy	3204	atggcagcccatctgaatcagagtatlaatgaatcccttaaagtctgaagcgtctaag	3257
Dd	3061	atggcagcccatctgaatcagagtatlaatgaatcccttaaagtctgaagcgtctaag	3114
RESULT 8			
AAFS7545			
ID	AAF57545	standard; DNA: 3114 BP.	
XX	XX	AAF57545;	
AC	AC		
XX	XX		
DT	DT	11-JUN-2001 (first entry)	
De	De	Human calcium channel alpha2delta subunit encoding DNA.	
KW	KW	Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;	
KX	KX	nervous system disorder; pain; epilepsy; anxiety; human; ds.	
OS	OS	Homo sapiens.	
XX	XX		
FH	FH	Location/Qualifiers	
FT	FT	CDS	1..3114
FT	FT		/*tag= a
PN	PN	MO200120336-A2.	
XX	XX		
PD	PD	22-MAR-2001.	
PF	PF	18-SEP-2000; 2000MO-EP09136.	
XX	XX		
PR	PR	16-SEP-1999; 99US-0397549.	
PA	PA	(WARN) WARNER LAMBERT CO.	
PI	PI	Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;	
DR	DR	WPI: 2001-257902/26.	
DR	DR	P-PsDB; AAB62242.	
PT	PT	Competitive binding assay for screening ligands which bind a cerebral	
CT	CT	cortical voltage-dependent calcium channel alpha2-delta-1 subunit,	
TT	TT	where the ligands identified are useful for treating disorders of the	

[illegible]

OY	864	tgccgagaaacccggaataatggtatcaatccagcgagcaacttcttcgaaaga-vgtgcatttta	923
Dp	721	tgccgagaaacccggaataatggtatcaatccagcgagcaacttcttcgaaaga-vgtgcatttta	780
OY	924	gttaacgttcagtgctgcagatcgaaagaaacccgtctgcactatcggaacgaacgtctca	983
Dp	781	gttgcagctcagtgctgcagatcgaaagaaacccgtctgcactatcggaacgaacgtctca	840
OY	984	tcacatttggatacacttggggatgaatgaactcttcacaaatattgtctataatgagagag	1043
Dp	841	tcacatttggatacacttggggatgaatgaactcttcacaaatattgtctataatgagagag	900
OY	1044	cttcaactatgttgaaacctgtgcctgaatggaacttgggtgcaagccgcagacagacaacaa	1103
Dp	901	cttcaactatgttgaaacctgtgcctgaatggaacttgggtgcaagccgcagacagacaacaa	960
OY	1104	gagacacttcagggagagcctcgggacaacacttccgcgaagaagattggaaatttggatata	1163
Dp	961	gagacacttcagggagagcctcgggacaacacttccgcgaagaagattggaaatttggatata	1020
OY	1164	gctcttgaaatgaaggcccttcaacaacttcgagtgatattcaaacacagcggaagagatgc	1223
Dp	1021	gctcttgaaatgaaggcccttcaacaacttcgagtgagtgatttcaaacacagcggaagagatc	1080
OY	1224	tgcaagtcagggccatcatgctcatbaactgtaatggggcgggtgagacactatgaataacctt	1283
Dp	1081	tgcaagtcagggccatcatgctcatbaactgtaatggggcgggtgagacactatgaataacctt	1140
OY	1284	gcgaataatacaatttggccagatgtgaaaggtttgcacattcaacttatttggacggagag	1343
Dp	1141	gcgaataatacaatttggccagatgtgaaaggtttgcacattcaacttatttggacggagag	1200
OY	1344	gctcgcgttgcagacaacaatccaaaggttgatgctgctgtgcacaagaagatlttttaccag	1403
Dp	1201	gctcgcgttgcagacaacaatccaaaggttgatgctgctgtgcacaagaagatlttttaccag	1260
OY	1404	atctccacacttggctgaatgtgcagaggaatgtcatatgaaataccttcacgtcttaacgg	1463
Dp	1261	atctccacacttggctgaatgtgcagaggaatgtcatatgaaataccttcacgtcttaacgg	1320
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Dp	1321	ccccaataatctgaaacccaaggagcatatgtgtgtgtgtgagccgaaagcttkaattgacagca	1380
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Dp	1381	ctgcactgatcatcagggccccgcctcgtatgcacacgtgatgcacatgctgcgttttaagag	1440
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Dp	1441	cagaaacgaacccaagatctgaaagggcattcttctctggagatggttgcgaa-agaatgtccca	1500
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Dp	1501	aaagaatactctgaaagacatcccccaatacaagtttagggatlttcagatgttagtgcatttgg	1560
OY	1704	atcccaataatgrrtatatccctgcgaagcgtcccggaactcgaagctgc-vgtaacgaagaaga	1763
Dp	1561	atcccaataatgrrtatatccctgcgaagcgtcccggaactcgaagctgc-vgtaacgaagaaga	1620
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Dp	1621	aaaaaagcgaaaggaacctaactaactaagtgatgcgtttgacacttccgaaagcggaatgga	1680
OY	1824	cgaaatgtaacgtgttggagaataatgctatggtgaatcgaaagaacgggggaagtlttccatgag	1883
Dp	1681	cgaaatgtaacgtgttggagaataatgctatggtgaatcgaaagaacgggggaagtlttccatgag	1740
OY	1884	gtggaagaagacagtggtgcgaaggaacggggttttggatgaacaaatgactactattat	1943
Dp	1741	gtggaagaagacagtggtgcgaaggaacggggttttggatgaacaaatgactactattat	1800
OY	1944	acagacatacaagggtaactcttcaattttagtgtgtgcttccacagaggtcatgtggaa	2003

Dp	1801	acagacacccaagggggtactcccttccagtttgaagtgctgctgtcccaaggtcaltgaggaa	1860
Oy	2004	tattttctccagaggaatgtaaccactcgaaagaagccgcgtgacttagaacatcccgat	2063
Dp	1861	tatttctccgagggaaatgtaaccactgaaagaagccgtgcactgacttagaacatcccgat	1920
Oy	2064	gtgtccctgtagagatgaaatgtgtctactgtgcaaacctgtgacccctagaccgacat	2123
Dp	1921	gtgtccctgtagagatgaaatgtgtctactgtgcaaacctgtgacccctagaccgacat	1980
Oy	2124	ctgttctcagtttagaagcgattaaagctctactctaaaggccaagaactctgtctccagt	2183
Dp	1981	ctgttctcagtttagaagcgattaaagctctactctaaaggccaagaactctgtctccagt	2040
Oy	2184	gataaagaattgatacccaagaagctctttttgaacgcgtgtgtgtgagtgcccccatggaagcg	2243
Dp	2041	gataaagaattgatacccaagaagctctttttgaacgcgtgtgtgtgagtgcccccatggaagcg	2100
Oy	2244	tatttgaccagccttgycacctcaacaacatctgaaaatcttgacaagggcggtgaggtgtgcc	2303
Dp	2101	tatttgaccagccttgycacctcaacaacatctgaaaatcttgacaagggcggtgaggtgtgcc	2160
Oy	2304	ttctctcgcaactcgcaaggcctctccagaatccaactgtttgtccggggtctgagcagctc	2363
Dp	2161	ttctctcgcaactcgcaaggcctctccagaatccaactgtttgtccggggtctgagcagctc	2220
Oy	2364	accaatcagagcttccctttaaagctctgtagcaagaaggaaacatttttaacgcagaccatttc	2423
Dp	2221	accaatcagagcttccctttaaagctctgtagcaagaaggaaacatttttaacgcagaccatttc	2280
Oy	2424	cctctctgtacccgaaagcgccgtctgtagcagaatctccaaaggagcttcgtctactgcataccca	2483
Dp	2281	cctctctgtacccgaaagcgccgtctgtagcagaatctccaaaggagcttcgtctactgcataccca	2340
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Dp	2341	ttcagcactgtgacccagttcaataaagaagcaatgtgtgtgacagcagatcaatccacagctc	2400
Oy	2544	ctgagcttgaaacggaatctccctggtgtgtgtagcagctgttagagcatctcagatgaaactgtgaatt	2603
Dp	2401	ctgagcttgaaacggaatctccctggtgtgtgtagcagctgttagagcatctcagatgaaactgtgaatt	2460
Oy	2604	ttccaaagaagagttctgtgactgtccgcagcagaacagttgtgtctccctgtgaaatgtgtcc	2663
Dp	2461	ttccaaagaagagttctgtgactgtccgcagcagaacagttgtgtgtctccctgtgaaatgtgtcc	2520
Oy	2664	atcacgctgtgatgatgtagaactgtgaaatgttaacctcatagacaataatgatatctttg	2723
Dp	2521	atcacgctgtgatgatgtagaactgtgaaatgttaacctcatagacaataatgatatctttg	2580
Oy	2724	gtgtcttgaaagcttaacacacagactgtgaaactttttgtgtgagatcggaggggcggtgatg	2783
Dp	2581	gtgtcttgaaagcttaacacacagactgtgaaactttttgtgtgagatcggaggggcggtgatg	2640
Oy	2784	aacaacatgtcctaacaatgtggtcctctttaaagaattaacctttagactaaccaagcagatg	2843
Dp	2641	aacaacatgtcctaacaatgtggtcctctttaaagaattaacctttagactaaccaagcagatg	2700
Oy	2844	tgtagagccaacaagaaggaaagcagcgaatggtgcgccatgtgctccctgtgaaacttaaatgccc	2903
Dp	2701	tgtagagccaacaagaaggaaagcagcgaatggtgcgccatgtgctccctgtgaaacttaaatgccc	2760
Oy	2904	ttcctctctgcaatgataatgtgatactatgcaacaaactgtgctgtctccctgtgtgaaatttaac	2963
Dp	2761	ttcctctctgcaatgataatgtgatactatgcaacaaactgtgctgtctccctgtgtgaaatttaac	2820
Oy	2964	ctctcagttgtgtgtagctccgatatactgacaagctaaagcccgaaattgaaacacacacctg	3023
Dp	2821	ctctcagttgtgtgtagctccgatatactgacaagctaaagcccgaaattgaaacacacacctg	2880
Oy	3024	gagccttgtgatactgaaatattccagcattgtctctgtgagcgacacatcctaagagagatac	3083

OY	1044	cltccactaigtvgaaaccttgctcgaaatgtgaacttvtgtcgaagccogaacagaaacaaaa	1103
Db	901	 cttccactaigtvgaaaccttgctcgaaatgtgaacttvtgtcgaagccogaacagaaacaaaa	960
OY	1104	gagcaactcagagagacatcgtgcgaacaacttctgcgaagaagattggaagtgtgacata	1163
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OY	1164	gctctgaaatcgagcccttcaacaactctgagtgatctcaaccacaacgggaacaagaaatc	1223
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OY	1284	gcaaaatacaaatctgacgaagatcgaaaggtctgcgaatctccacatacctcatctgagag	1343
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Db	1321	cccaaaatcatcgacaagagacatgaatgtgtgtgtgtagaccgaaccttmacatgtgacgact	1380
OY	1524	ctgacactgagatcgaagccctgtccctgagacacagctgagccatgtgcctgtgttaagaag	1583
Db	1381	ctgacactgagatcgaagccctgtccctgagacacagctgagccatgtgcctgtgttaagaag	1440
OY	1584	cagaaacgaaacacgaatcgaagagcattctctcttgtagagttgtcttgacaaagatgtccagtg	1643
Db	1441	cagaaacgaaacacgaatcgaagagcattctctcttgtagagttgtcttgacaaagatgtccagtg	1500
OY	1644	aaagaactcttgaaagccatccccaataacaaatagtgagatcaacgtatagctcttgca	1703
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Db	1621	aaaaagcgaaggaacctaactatagtaagcgttgacccctctgaggttgagatgtagaagac	1680
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OY	1884	gtgaaagaaagacgttgagacaagaaggaacggtttcttgtagatgcacaatgtactatat	1943
Db	1741	gtgaaagaaagacgttgagacaagaaggaacggtttcttgtagatgcacaatgtactatat	1800
OY	1944	acagacatacaaggtctactccttccagtttaagtggtgagccttcccaaggtcatgaggaaa	2003
Db	1801	acagacatacaaggtctactccttccagtttaagtggtgagccttcccaaggtcatgaggaaa	1860
OY	2004	tatttctccgagggagatgtaaacacacgaagaagggcctgtgatgacitagaagatcccgat	2063
Db	1861	tatttctccgagggagatgtaaacacacgaagaagggcctgtgatgacitagaagatcccgat	1920
OY	2064	gtgtcctctggcagatgaaatggtctctactgtcacacatgacactacacacctgtgacacggcat	2123
Db	1921	gtgtcctctggcagatgaaatggtctctactgtcacacatgacactacacacctgtgacacggcat	1980

QY	2124	ctgtctcagttgaagacgatttaagctcttaaccttaaaagcgaaagacccctgtctcagtg	2183
Db	1981	ctgtctcagttgaagacgatttaagctcttaaccttaaaagcgaaagacccctgtctcagtg	2040
QY	2184	gataaagatttaaccagaagctcctcttttgacgagctgtgtgagtgcccccttgaagcg	2243
Db	2041	gataaagatttgaatccagaagctcctcttttgacgagctgtgtgagtgcccccttgaagcg	2100
QY	2244	tattgacacagcttgcctccaacaatctgtanaaaattctbnaaagcgctgtgaagctgc	2303
Db	2101	tattgacacagcttgcctccaacaatctgtanaaaattctbnaaagcgctgtgaagctgc	2160
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QY	2784	aacaaattgtctaacaatgvggtcctttaaagaattacccttatagtactacaagcattg	2843
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1861 tatcttccgaagggaatgttaaccatcgaaagagcgctctgacatgacttaagacatcccgat 1920
2064 ggtgctcttgacgaatgaatgtgtctactctgaacacgtgacttaaccccttgacacgcat 2123
1921 ggtgctcttgacgaatgaatgtgtctactctgaacacgtgacttaaccccttgacacgcat 1980
2124 ctgtctcagtttagaagcgatttagcctctactaactaagaagcgaaagactctgtccagtgat 2183
1981 ctgtctcagtttagaagcgatttagcctctactaactaagaagcgaaagactctgtccagtgat 2040
2184 gataaagaattgtatccaaagaagtccttcttgaacgctgtgtgtgtgtgtgtgtgtgtgtgt 2243
2041 gataaagaattgtatccaaagaagtccttcttgaacgctgtgtgtgtgtgtgtgtgtgtgtgt 2100
2244 tatgtgaacagcctgtgcctctcaacaatctgaaatctgcgaacgagctgtgaggtgtgc 2303
2101 tatgtgaacagcctgtgcctctcaacaatctgaaatctgcgaacgagctgtgaggtgtgc 2160
2304 ttctctcgacatcgacacgagcgctctcagaatcaacgtgtgtgtgtgtgtgtgtgtgtgtgt 2363
2161 ttctctcgacatcgacacgagcgctctcagaatcaacgtgtgtgtgtgtgtgtgtgtgtgtgt 2220
2364 accaatcaggaactctcttgaagaagctgtgcgaacaaggaagaacattttaaicgagaacatcttc 2423
2221 accaatcaggaactctcttgaagaagctgtgcgaacaaggaagaacattttaaicgagaacatcttc 2280
2424 cctctctgtgatacgaagaagcgctgtgacagatltcccaaggagcgctgtgtctactcgatccca 2483
2281 cctctctgtgatacgaagaagcgctgtgacagatltcccaaggagcgctgtgtctactcgatccca 2340
2484 ttccagactgtgacacgtcaataaagaatgtgtgtgacagcaagtatcatcatccagctc 2543

|||||
Db 2341 ttccagactgtgacacgtcaataaagaacatgtgtgtgacagcaagtatacatccagctc 2400
Qy 2544 ctgatagaacggaataatctctgtgtgtgtgacgctgtgaagcatltcagatgaaactgaaatt 2603
Db 2401 ctgatagaacggaataatctctgtgtgtgtgtgacgctgtgaagcatltcagatgaaactgaaatt 2460
Qy 2604 ttccaaaggaagtctctgactgtccagacagacagtggtgtcttccctgagatgtgcaattgtcc 2663
Db 2461 ttccaaaggaagtctctgactgtccagacagacagtggtgtcttccctgagatgtgcaattgtcc 2520
Qy 2664 atcagctgtatgataagactgtgataatgtgttactctcaatagaacaataatgattattttg 2723
Db 2521 atcagctgtatgataagactgtgataatgtgttactctcaatagaacaataatgattattttg 2580
Qy 2724 gtgtctgaagaactacacacagactgtgagactttttgtgtgagatcgaaggagctgtgatg 2783
Db 2581 gtgtctgaagaactacacacagactgtgagactttttgtgtgagatcgaaggagctgtgatg 2640
Qy 2784 aacaatctgctaaacaatgtggtcctttaaagaattacccttatagtactacaaagcatg 2843
Db 2641 aacaatctgctaaacaatgtggtcctttaaagaattacccttatagtactacaaagcatg 2700
Qy 2844 tgtagagccacaagaaggaagcagatgtggtcccaatggtccctctggaatccttaataatgctc 2903
Db 2701 tgtagagccacaagaaggaagcagatgtggtcccaatggtccctctggaatccttaataatgctc 2760
Qy 2904 ttctctctctgacgtataaattgtatcatgacagaactgttctgtgtctgtgtgtgaaattaac 2963
Db 2761 ttctctctctgacgtataaattgtatcatgacagaactgttctgtgtctgtgtgtgaaattaac 2820
Qy 2964 ctctgcagctgt 3023
Db 2821 ctctgcagctgt 2880
Qy 3024 gaagctgtgataactgataatccagacatcgtctctgtgacgacacatcaaggaagactaca 3083
Db 2881 gaagctgtgataactgataatccagacatcgtctctgtgacgacacatcaaggaagactaca 2940
Qy 3084 gggataatgtctgtgtgaagaactgtcccaagctcttctgtatcatccagaatcccaagcagc 3143
Db 2941 gggataatgtctgtgtgaagaactgtcccaagctcttctgtatcatccagaatcccaagcagc 3000
Qy 3144 aacctgtctatgt 3200
Db 3001 aacctgtctatgt 3057

RESULT 11
AAA09260
ID AAA09260 standard; cDNA; 2008 BP.
XX
AC AAA09260;
XX
XX
DT 10-AUG-2000 (first entry)
XX
DE Human alpha-2-delta-C gene 3' splice variant.
XX
XX alpha-2-delta-C; calcium channel subunit; 3p21.1; gabapentin; cytosolic;
KW anticonvulsant; antimigraine; antiparkinsonian; antidepressant;
KW splice variant; ss.
XX
OS Homo sapiens.
XX
PN WO200020450-A2.
XX
PD 13-APR-2000.
XX
PF 07-OCT-1999; 99WO-US23519.
XX
XX 07-OCT-1998; 98US-0103322.
PR 30-OCT-1998; 98US-0106473.
PR 29-DEC-1998; 98US-0114088.


```
DB 1681 ggattccaggttatgcttccttgcaatcccaataatgatataatcttcagcattccggaac 1740
OY 1741 tcagcgctcgtatcgaagaagaagaacgcgaagaacctaactatcgtagcgtgacc 1800
DB 1741 tcagcgctcgtatcgaagaagaagaacgcgaagaacctaactatcgtagcgtgacc 1800
OY 1801 tctctgagtgagtgagggaagaccgagatgactgtttgaaataatgctatggtgaatcgaa 1860
DB 1801 tctctgagtgagtgagggaagaccgagatgactgtttgaaataatgctatggtgaatcgaa 1860
OY 1861 agacggggaagcttccatgagtgaggaagacagtgagcaaaagggaacgggttt 1917
DB 1861 agacggggaagcttccatgagtgaggaagacagtgagcaaaagggaacgggttttt 1917

RESULT 12
AAZ51626
ID AAZ51626 standard; cDNA; 1774 BP.
XX
AC AAZ51626;
XX
DT 21-JUN-2000 (first entry)
XX
DE Human membrane channel protein-10 (MECHP-10) cDNA.
XX
KW Membrane channel protein-10; MECHP-10; diagnosis; treatment; lymphoma;
KW cell proliferative disorder; bursitis; atherosclerosis; cancer; sarcoma;
KW inflammatory disorder; AIDS; Addison's disease; cystic fibrosis; asthma;
KW diabetes mellitus; osmoregulatory disorder; diarrhoea; renal failure;
KW muscular disorder; myocarditis; Duchenne's muscular dystrophy; nocturnal;
KW cardiovascular disorder; hypertension; bronchitis; vasculitis; cardiac;
KW neurological disorder; Alzheimer's disease; Parkinson's disease; human;
KW Huntington's disease; antiarteriosclerotic; hepatotropic; cytostatic;
KW anti-HIV; antianaemic; neuroprotective; immunomodulator; antidiabetic;
KW hypotensive; vasotropic; antiasthmatic; antiinflammatory; antidepressant;
KW anticonvulsant; thrombolytic; antiParkinsonian; immunostimulant; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 183..1742
FT FT /*tag= a
FT FT /product= "MECHP-10"
FT FT misc_binding 1275..1322
FT FT /tag= b
FT FT /bound_moiety= "Probe or Primer"
XX
PN WO200012711-A2.
XX
PD 09-MAR-2000.
XX
PE 02-SEP-1999; 99WO-US20468.
XX
PR 02-SEP-1998; 98US-0145815.
PR 12-NOV-1998; 98US-0191283.
PR 09-DEC-1998; 98US-0208821.
PR 26-JAN-1999; 99US-0237506.
PR 10-FEB-1999; 99US-0247891.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Au-Young J, Bandman O, Tang YF, Reddy R, Hillman JL, Yue H;
PI Lal F, Corley NC, Guegler KJ, Gorgone G, Baughn MR, Azimzai Y;
XX
DR MPI: 2000-256643/22.
DR P-PSDB; AAY70460.
XX
PT Novel human membrane channel protein and polynucleotide useful for
PT diagnosing and treating cell proliferative, inflammatory, secretory,
PT osmoregulatory, muscular, cardiovascular and neurological disorders -
XX
PS Claim 9; Page 124-125; 140pp: English.
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XX
CC The present sequence is a cDNA identified in Incyte clone 3148427
CC derived from ADRENON04 cDNA library. It encodes human membrane channel
CC protein-10 (MECHP-10), which is expressed in cardiovascular, endocrine
CC and nervous tissues. Anti-MECHP antibodies can be used as therapeutic
CC antagonists and reagents for diagnosis and monitoring diseases. MECHP
CC cDNA can be used for diagnosis of MECHP-related diseases and gene
CC mapping. MECHP can be used for treatment of cell proliferative disorders
CC such as bursitis and atherosclerosis, cancers like lymphoma and sarcoma,
CC inflammatory disorders like AIDS and Addison's disease, transport or
CC secretory disorders like cystic fibrosis and diabetes mellitus,
CC osmoregulatory disorders like diarrhoea and renal failure, muscular
CC disorders like myocarditis and Duchenne's muscular dystrophy,
CC cardiovascular disorders like hypertension and vasculitis, congenital
CC lung anomalies like bronchitis and asthma and neurological disorders like
CC Alzheimer's disease, Parkinson's disease and Huntington's disease.
XX
SQ Sequence 1774 BP; 539 A; 366 C; 440 G; 429 T; 0 other;
XX
Query Match 41.0%; Score 1545; DB 21; Length 1774;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 1614; Conservative 1; Mismatches 51; Indels 19; Gaps 2;
OY 252 ataccgctctccggtggaagctctgagccctgcttggtagggagataaatccatt 311
DB 8 ataccggtgaccgcggtcgtcgtggaagactcgggccttggtagggagataaatc 67
OY 312 gctcgaagtaactcgtgtcccaagcttcgcaagaatacgaagtaagaagaagac 371
DB 68 catgctgaataaccggttcccaagcttcgcaagaatacgaagtaagaagaagac 127
OY 372 gttccatagaaga-a-atgattgctcccaactcgtgtaagaagctgcaagaacatgca 430
DB 128 gttccatagaagaagactcgtatggtcccaactcgtgtaagaagctgcaagaacatgca 187
OY 431 agagatgtttacaagaagcttgaggccgtgacggtcgtgtgtagagtgagaagaagc 490
DB 188 agagatgtttacaagaagcttgaggccgtgacggtcgtgtgtagagtgagaagaagc 247
OY 491 acaccctgaacatgaattgattgacagacttaacatgaataactcaactcgtgtgcat 550
DB 248 acaccctgaacatgaattgattgacagacttaacatgaataactcaactcgtgtgcat 307
OY 551 aatgtaagggacaagaacgggaatttttgtagctgggaagaatcatcttagcccc 610
DB 308 aatgtaagggacaagaacgggaatttttgtagctgggaagaatcatcttagcccc 367
OY 611 aatgacattttaattatgttgcttggaacatgaactgaagtgaagtcgaagtcacac 670
DB 368 aatgacattttaattatgttgcttggaacatgaactgaagtgaagtcgaagtcacac 427
OY 671 gaacatgtacacaagaacccctgcaatgtcgaatgaggtttatggttcgaatctcaaa 730
DB 428 gaacatgtacacaagaacccctgcaatgtcgaatgaggtttatggttcgaatctcaaa 487
OY 731 caaagttttgtagataactttgacgcgtgacacatcttcataatgcaagtaactttgaa 790
DB 488 caaagttttgtagataactttgacgcgtgacacatcttcataatgcaagtaactttgaa 547
OY 791 tgcagaagggcttttttgagcagatccgggagatgaatgggaacgaatggaatgaggt 850
DB 548 tgcagaagggcttttttgagcagatccgggagatgaatgggaacgaatggaatgaggt 607
OY 851 catgctctgactgcaggaacccgaataatgtatccacgacgaacacttccgaaga 910
DB 608 catgctctgactgcaggaacccgaataatgtatccacgacgaacacttccgaaga 667
OY 911 cgtggtcaattttagttgaagtcagtcagtcagcaatgaagaagactccgtctgactatcgaa 970
DB 668 cgtggtcaattttagttgaagtcagtcagtcagcaatgaagaagactccgtctgactatcgaa 727
OY 971 gcaaacgctccatcatttggatataacttgtagatgagtagacttccaacataattgc 1030
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Db 728 gcaaaagctcaccattcttgatcacacttgaggatgacatctcttcaacataatgctc 787
OY 1031 ttaataaggagactcactatgtgaaaccttcgctgaatgtaactttgttgaagccga 1090
Db 788 ttaataaggagactcactatgtgaaaccttcgctgaatgtaactttgttgaagccga 847
OY 1091 caggacaacaaagagacttcaggagacatctgacaaaccttcgcacaaagaaatttg 1150
Db 848 caggacaacaaagagacttcaggagacatctgacaaaccttcgcacaaagaaatttg 907
OY 1151 aatgttgatatagtctctgaataaggcttcaacattctgaagatattcaaccacggg 1210
Db 908 aatgttgatatagtctctgaataaggcttcaacattctgaagatattcaaccacggg 967
OY 1211 acaagaaatatactcagtcagtcagccatcagtcacataactgagggcggctgagacacta 1270
Db 968 acaagaaatatactcagtcagtcagccatcagtcacataactgagggcggctgagacacta 1027
OY 1271 tgaatacaatcttgcaaaataacaaatctgagccagatcgaaaggttcgacattcacaatacct 1330
Db 1028 tgaatacaatcttgcaaaataacaaatctgagccagatcgaaaggttcgacattcacaatacct 1087
OY 1331 catgagacgagagagcgctgttgacagacaatctcaaaagtgaatgtgctgtgacacaaagg 1390
Db 1088 catgagacgagagagcgctgttgacagacaatctcaaaagtgaatgtgctgtgacacaaagg 1147
OY 1391 attcttaccagaaatctcacccttgctgagtgctgagagaaatgcatgaaataccttca 1450
Db 1148 attcttaccagaaatctcacccttgctgagtgctgagagaaatgcatgaaataccttca 1207
OY 1451 cgtgtctagccggcccaaaatgcatcgacagagacatgagtgtgtgagacgaactta 1510
Db 1208 cgtgtctagccggcccaaaatgcatcgacagagacatgagtgtgtgagacgaactta 1267
OY 1511 catgagacgagact-----ctgactgaatgatacgaaggcccgctctgata 1552
Db 1268 catgagacgagactcctccctcagggcacaagaagctgacatgatacgaaggcccgctctgata 1327
OY 1553 gacacatgtatgacatctgctgtgtttagtaagcagaacgaacacagatcgaaaggacattct 1612
Db 1328 gacacatgtatgacatctgctgtgtttagtaagcagaacgaacacagatcgaaaggacattct 1387
OY 1613 tctggagagtggtgtgacacagatgtcccaatgtaaaagaactctgaaagacacatcccaata 1672
Db 1388 tctggagagtggtgtgacacagatgtcccaatgtaaaagaactctgaaagacacatcccaata 1447
OY 1673 caagttagagatcaacggttatgctcttgcacatcacaaataatggttatatctctgacga 1732
Db 1448 caagttagagatcaacggttatgctcttgcacatcacaaataatggttatatctctgacga 1507
OY 1733 tccggaactcagagctgtctgtaacgaagaagaaagcgaaagaaaccttaactatagtag 1792
Db 1508 tccggaactcagagctgtctgtaacgaagaagaaagcgaaagaaaccttaactatagtag 1567
OY 1793 cgttgacccctctcgaagtgtgagtgggaaagacgagatgacgtgttgagaatgtctatgct 1852
Db 1568 cgttgacccctctcgaagtgtgagtgggaaagacgagatgacgtgttgagaatgtctatgct 1627
OY 1853 gaaatcgaaagacgaggaattttccatctgagtgagtgtaagaagacagtgacacaaaggaacg 1912
Db 1628 gaaatcgaaagacgaggaattttccatctgagtgagtgtaagaagacagtgacacaaaggaacg 1687
OY 1913 ggtctt 1917
Db 1688 tttttt 1692

RESULT 13
AAS17582
ID AAS17582 standard; cDNA; 3345 BP.
XX
AC AAS17582;

XX 26-FEB-2002 (first entry)
DT
XX
DE DNA encoding novel secreted protein #11.
XX
KW Secreted protein; cytosolic; immunosuppressive; vulnary; vaccine;
KW antiinflammatory; neuroprotective; nephrologic; cardiovascular;
KW human; cancer; autoimmune disease; wound healing disorder; infection;
KW haematopoietic disorder; inflammatory disorder; infertility;
KW neurological disease; psychiatric disease; cardiovascular disease;
KW respiratory disease; renal; gastrointestinal; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..3345
FT /tag= a
FT /product= "Human secreted protein"
XX
PN WO200179454-A1.
XX
PD 25-OCT-2001.
XX
PE 11-APR-2001: 2001WO-US11797.
XX
PR 13-APR-2000: 2000US-196603P.
PR 24-APR-2000: 2000US-199417P.
XX
PA (SMK) SMITHKLINE BEECHAM CORP.
PA (SMK) SMITHKLINE BEECHAM PLC.
XX
PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
XX
XX WPI: 2002-061975/08.
XX P-PSDB: AAU09870.
PT New secreted proteins or polypeptides, useful for treating e.g. cancer,
PT autoimmune diseases, wound healing disorder, infections, haematopoietic
PT disorders, inflammatory disorders, infertility, cancer
XX
PS Claim 2; Page 42-44; 92pp: English.
XX
CC The invention relates to an isolated novel secreted polypeptide (I) and
CC polynucleotide (II). (I) and (II) are useful for treating cancer,
CC autoimmune diseases, wound healing disorder, infections, haematopoietic
CC disorders, inflammatory disorders, infertility, neurological and
CC psychiatric diseases, cardiovascular diseases, respiratory diseases,
CC renal diseases, or gastrointestinal diseases. These may also be used to
CC treat diseases, abnormalities and disorders caused by abnormal
CC expression, production, function and/or metabolism of the genes, as
CC vaccines for inducing immunological response in a mammal, and in
CC screening methods for detecting the effect of added compounds on the
CC production of mRNA and polypeptide in cells. The polypeptides can be used
CC as immunogens to produce antibodies immunospecific for the polypeptides,
CC and to identify membrane-bound or soluble receptors. The polynucleotides
CC may be used as diagnostic reagents, in chromosome localisation studies,
CC and in tissue expression studies. The present sequence represents the
CC coding sequence of novel human secreted protein #11.
XX
SO Sequence 3345 BP; 772 A; 943 C; 960 G; 670 T; 0 other;

Query Match 33.6%; Score 1268.2; DB 24; Length 3345;
Best Local Similarity 63.8%; Pred. No. 9,9e-278;
Matches 2010; Conservative 0; Mismatches 1118; Indels 21; Gaps 5;

OY 250 agataccgtctcctgctggaagactctgggctctgtgtgtgagataaatcca 309
Db 161 agatctcttggaagacgtaagctatggctcagcacttcggcgagacctgtataaca 220
OY 310 ttgctgtaagtaactcctgcttccagctctctgcaaaagaatacagaatgtagaagaag 369
Db 221 cgtgaccaaataactcagctctctctctgctgacagaagaatcaagaatgtggaatcca 280

OY	370	acgtltyccatagaaagaaatttgatggtcctccaaactggtlaaagaagctgtgcacaaagaaatc	429
Db	281	gtctgaagatcagaaagagttgtagtgccttgagctgtggtgaggaattcttcagagagatc	340
OY	430	aaggaatgtttcacaagaanaatctgaaagccgtccagagcgtctgtgtgagagctgcagaagaag	489
Db	341	agaacatagctgcgagagaaagatcgaagcggtccagaatactgtgtggaactgtccgagagag	400
OY	490	cacacgtgaaacaacgaatattgtagtcgagacttacagaatgaataatcttcacatgtgtgcga	549
Db	401	ccgagccgtgaacccaagaaattcaatgaaatccctgtgtgttcgactattacaaactcgtgccga	460
OY	550	taaatgaaagagaaacaagaacgagggaatttttttgagctgtggaagaagaaatctcaattagccc	609
Db	461	tcaacgagagaggacgagaaagggcaacttcgtgagctgtgagctgtgscgcgaagtctccctcgaggt	520
OY	610	caaatgaccattttaaataatttgcctgtgaacatcaatcagtttaagtgaaagtccaagtacca	669
Db	521	ccaattgtccacttcaagaacaacctgcggtgaaacccctccacatcgacagcgttgcagctgtccca	580
OY	670	cgaaactgtcaacaanaagaccctgcgcaattgtcaattgggtttatgtggcttcgaattccaa	729
Db	561	ccaaacgtgatacaacaagaacccagaataattttaaataatgaaatcacaatgtccgtgaacgttga	640
OY	730	acaaagattttgtatgaataactttgacacgttgaaaccatctcatalgtgagtagtaacttggaa	789
Db	641	atgctgtccttcgtgaggaacttccagagagaccacaagttgcacctgagcaaatatttggca	700
OY	790	gtgcgaagggcctttttaaggcaatgccggggaattaaatggaacccaatgagaatgag	849
Db	701	gtgcgaactggaattcttcaagatctcattccagatgataaataatggaacactgatatgagaatgag	760
OY	850	tcattgtccttcgactgtcgaagaaacccaagaataatggaataccaaagcagaactcttcgaaag	909
Db	761	tcattcaacttttgagatccggaacccgcggtgtgaaacttcaatcagctgtcactcttcccaag	820
OY	910	acgtggtcattttttagtgcagctgcagtcgagcagatgaaagaagactccgtctgatactcagga	969
Db	821	acatagtgatttttgggtgagcgtgagcggaatgagatgaaagggcgtgaggaatgactattggca	880
OY	970	agcaaacagttcattccatttttgatacaacttggggatgaaatgactcttcaacataattg	1029
Db	881	agcacacatcaacccaactcttggacaacctgtgggagagaatgacttcaataatcatag	940
OY	1030	cttaataatggagagcttcaactatgtagtggaaacttgccttgatgaaacttgtgtgcagaagc	1089
Db	941	cgtaacatgactaagctccattatatactgaagccttgttttaaaaggatccctcgtcccgagg	1000
OY	1090	acaagacaacaagaagaaacattcagaagagcatcttgagacaacattttgcgcaagaagattg	1149
Db	1001	accgagacatcagagagacatcttcaactctcgtgtgaggaagtgtgataatgttcaaaagtgtg	1060
OY	1150	gaatgttggatataagctctgaaatgagggccttcaacattcttgatgaaatttcaaccaacag	1209
Db	1061	gggtcgtggaaccaagcccttgagagaaagccttccagatcctgaaagcaagtcccaagggca	1120
OY	1210	gacaaggaatgatactgagtcagcgccaatgctctataactgaatggtgcgtgtgacacct	1268
Db	1121	agcaagaagaagcctcttgacaacagagccatcatgcttccatccgaacggtgacgtgtgagagact	1180
OY	1270	atgatacaatcttggcaaaatatacatgtgcgaagatcgaagaagtttcgatcttcaataacc	1329
Db	1181	acggagccggtgtttggaagaagtataactgtgcagaactgtaagtctccgaagtcttcaactacc	1240
OY	1330	tcattttacgagagagcgtgcgttttggcagacaatctaaagatggaatggtcgtgtgcacaag	1389
Db	1241	tcatttggagagagagtgctttttgtgcaccgcatgaaagtgttgatcatgcaacaacaag	1300
OY	1390	gattttttaccagatctccaaactgtgcgtgatagttgcagagaatgtcatggaataccttc	1449
Db	1301	gtctactacaacgaatctcaacgctctgtgcgagaccccaaggagaagctgaaatggaatcttcgc	1360

QY	1450	acgtgtcattagccggccccaagtatcatccgacggagagcatgtgtgtgtgtgtgcgcaagctt	1509
Db	1361	agctgttcacgcccgcctatgtgtatccaacacgcagccacgatcatctgtgtgcagaagtcctt	1420
QY	1510	acattgcacgacgtct-----gactgtgtatcagagggcccgcttcctgtgtgacacgtttag	1563
Db	1421	acattgcacgacgacgtcctcctcagcttcgcaggtccagagccgtgcacatgtctccacacgttgg	1480
QY	1564	ccatctcgtgtgtttagtaagcgaagcaacgaatctgcgaaggtgcattctctgttgagatgg	1623
Db	1481	ccatgtccagctctcgaagcaagaagcaacgcaatcccatcagtgcatcttctcgtgtgtgtg	1540
QY	1624	ttgtgcacagatgtcccgatgtaagaactcttctgaagaccatccccaataacagtttaaggga	1683
Db	1541	tgtggtctcagatgttggccctgtgagatgtctgtatgaactgtgtgcccgtgtacaaagcttggag	1600
QY	1684	ttcaaggttatgtccttgcataccaataatgtgtatatcctctgaagcatgcgatccggaactca	1743
Db	1601	tgcacggaataagccttctctgaacaccacaatgtgcatactctcccatcccgacccctc	1660
QY	1744	ggctcgtctagcaagaaggaanaaagcgca---ggaaacccatactatagtcgtttgac	1800
Db	1661	ggccctcgttgcacagaggtgggaagaaactaaacccaacccaactacatacaacagttgtgattc	1720
QY	1801	tctctgtaggttggagtgtgtgtgaagacgcgaagatgtctgtgtagaatgtctatgtgtgacatgaa	1860
Db	1721	tctccgaagtgtgagtgtgtgtgaagacagagctgtgaattctctgtgaacagcattgtatcaatagg	1780
QY	1861	agaacgggggaagtttcccatctgtgtgtgtgtgaaggaacagctgtgtacaagaagggaaggttttg	1920
Db	1781	aaacaggtatctctccgtatgtgagtgtgaaggttccgaatgtgataaagggtgaagagttcttc	1840
QY	1921	tgatatacaatatacactatctatatacagacatcaaaaggtacccctctcagttctgaattgtgtg	1980
Db	1841	tctgtacccaatgtactactcttctcaagagacatcagagaaaccccttcagttctgtgtgtgtg	1900
QY	1981	cgcttccagaggtcatgtgtgaataatctctctccgaagggaatgtatcaacatcgaagaagccc	2040
Db	1901	tgtgttcccggtggccagagatacatccttctgtgtggaacaacgtctgtgtgaagaagcgcc	1960
QY	2041	tgcattgacttaagaatcccgatgtgtgtctctgtgcagatgaatgtgtccctacgtgcaaacctg	2100
Db	1961	tgcattgacttgccttaccacgaagccctgtgcccctgtgcgtgtgactgtgattctactcgtacatcaag	2020
QY	2101	acctaacacctgaagacccgcatactgtctccatgttgtaagagcattaagcttactactaaag	2160
Db	2021	aatatgaccccaagacaacccggaaggtccacgcagctctatgtatgtatgcattgtccgtctctcatcca	2080
QY	2161	gcacaaagacctctgtctccagtgtgtataaagaattgtatccaaagaaagtcctctttttgacggtg	2220
Db	2081	ggaaaggaaccagaaactgtgagtgtgtgacgtgtgagctgtgtccggagagtggtgttttagcggtg	2140
QY	2221	tgtgtatgtgtcccatcttgaagtgctatgttgacaagcctgtgtccctcaacaactctgaaatc	2280
Db	2141	tgtgtacaaacccccaatggaagctactctgtgacagcgtctgtgacctaaacatgtgtccgaagagtt	2200
QY	2281	cgtgaacaaggtgtgtgaaggttgccttccctccgcgaacatcgtgcagcggtcctccacgaatcaacc	2340
Db	2201	ctgaaacagctgtgtgacatagtccttccctcgtgtggaacccggtcgtgtcctctgtgaagacagct	2260
QY	2341	tgttgttgcgggtgtgacagcttcaaccaaatcagagaaattctctgtaaagctltgtgcgaacaagaga	2400
Db	2261	tgttgcgtgtgtgtccgtgtgtcgcgaacagagttctctgtacaaactgtgagacagagcca	2320
QY	2401	acatttttaagcgagaccaatttccctctctctgtgtacgaaagagccgctgtgagcgaagttccag	2460
Db	2321	gggtgttccacccctgtgacacgcttcccgctgtgtgtatccgcgaaggtcctcagagatcatctgtgtg	2380
QY	2461	ggaggttctgtctactcgtatcccatcagcagacgtgtgacagta-----ataaagacatg	2514
Db	2381	ggaggttctgtcttcaacctctcgtctgtgtgcgaagaagccccaagaatgtgcgggtgtaaacctatgtg	2440
QY	2515	tgtgtacagcaagtatcatcatccagcttctgtgtatgaacggaanaatctccttltgtgtgtcag	2574

DB 2441 tggtagcggcaagcacagctggtgacccgtagacaagagacagccattgctgcag 2500
OY 2575 cgttaagccttcaagatgaactgtaatttttccaagaagatctgacgagcagagac 2634
DB 2501 ccgagggcttccaatgaaagctggaattccctcagcagcaattctggcggaacgcgac 2560
OY 2635 agtgcctccctggaatggcaaaatgctcacaacgctgtgaatgaatgactgtgactgtt 2694
DB 2561 agtgcagcaactgtggaatggcgctgcacacagagctgcgagagcaatgactgtgactgt 2620
OY 2695 acctctaaacaaatgaatgaattatttggctgtcgaagaactcacaacagactgcagact 2754
DB 2621 tgcgtacacacaacaaaggttcaattctgaatcccaagaggtcccgagagacgaggaat 2680
OY 2755 ttttctgtagatcggagagctgtgtagaacaattgcaacaattgcaacgctctctttaa 2814
DB 2681 tctctggggaaggtggaatggtgtgctgtcctgaacagctgtcagcaatggggtgttca 2740
OY 2815 gaattacccttaatgaatcaacaaatgtagagccaagaagaaagcagcagtgagc 2874
DB 2741 aagtgcactatgtagactacagcaltgcaaaccttcagagtagcaaccacagtgagc 2800
OY 2875 cccatggtcctctggaatcctttaaagcttccctcctgcagtaaaatgataatgacag 2934
DB 2801 cccagcccttggtagcagcccaattctcgtccttgaagcgacaaagtggtgtgtgcag 2860
OY 2935 aactgtctctgtagcgtggaatttaactctcgtcagtttggtagcagctccagatagac 2994
DB 2861 agctgtgtgtgtctcctcgtgaggtgagtgctgtggtcctcgtgtcagacagaagggc 2920
OY 2995 ctaaaagccagaatgtaacaga---ccctggagcctctgtggaatgaatcagacat 3051
DB 2921 agggccacaacaacagaagcagagaccgctgcagccctggagcagaggtaccctgtg 2980
OY 3052 tggctcctgagggcacaatcagaagagactacaggggaatttgcctgtgaagaatgtctca 3111
DB 2981 tctgtgaacagcggcgaatccggagagcgaagcagtgatcgtggatgctgggctgtccaga 3040
OY 3112 agtctcttgcataccgaatcccaagcagcagcctgtcagtggtgtgtagaagca 3171
DB 3041 aggtatttggtagcagcagatcccaagatgaactcctcctcctcgtggagacagccca 3100
OY 3172 gctgcctctg---tgaattctgtggcccatcacacatggaaccattgaatcaagtata 3228
DB 3101 cctctgcagaaatgggctcgtgtcctgagatattgaccttaagaagtggtctgcacata 3160
OY 3229 atgaatcccttaagtgtagaagcttcaagggcccaagaagatcagaagcgcccaaatctt 3288
DB 3161 atgctctctgtaaaatgtagcagggatgctcccaagaagctcccgcgagcagactcct 3220
OY 3289 gtcagtcttcaatccctgaggaatgtagcagggagtggtggggtgcgagcagatctcaag 3348
DB 3221 gtcacgctctcatcacaagaggaagatgcccagagactgcgagcgtctggaacactcag 3280
OY 3349 cccagaagatcctcctctcgtcctcctg 3377
DB 3281 cctgcgcgcctcactcctgctgctgtg 3309

RESULT 14
AAA09254
ID AAA09254 standard: cDNA; 5073 BP.
XX
AC AAA09254;
XX
DT 10-AUG-2000 (first entry)
XX
DE Human alpha-2-delta-D gene.
XX
KW alpha-2-delta-D: calcium channel; 12p13.3; gabapentin; cytostatic;
KW anticonvulsant; antitrigemine; antiparkinsonian; antidepressant; ss.
XX

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 3..3365
FT /tag= a
XX
XX MO200020450-A2.
XX
PD 13-APR-2000.
XX
PF 07-OCT-1999: 99WO-US23519.
XX
PR 07-OCT-1998: 98US-0103322.
PR 30-OCT-1998: 98US-0106473.
PR 29-DEC-1998: 98US-0114088.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Johns MA, Moldover B, Offord JD:
XX
DR WPI: 2000-303744/26.
XX
DR P-PSDB: AAY92321.
XX
PT New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
PT proteins, useful in the treatment of epilepsy, migraine, chronic pain,
PT anxiety, multiple sclerosis or cancer
XX
XX
XX Claim 1, Page 64-66; 88pp; English.
XX
PS The alpha-2-delta-D gene encodes a calcium channel subunit polypeptide.
CC The gene has been mapped to chromosome 12p13.1. This gene and the related
CC alpha-2-delta-C and -B genes are useful for protecting mammalian cells
CC from abnormal calcium flux by introducing expression vectors containing
CC the respective gene into mammalian cells. The antisense genes are also
CC useful for treating or preventing epilepsy. The alpha-delta-2-A protein
CC is a high-affinity binding target of the anti-convulsant drug gabapentin.
CC Therefore, alpha-delta-2 proteins may also be targeted to treat
CC seizure-related syndromes, migraine, ataxia, vestibular defects, chronic
CC pain, sleep interference, anxiety, amyotrophic lateral sclerosis (ALS),
CC multiple sclerosis, mania, tremor, parkinsonism, substance abuse or
CC addiction syndromes, mood, depression or cancer.
XX
SQ Sequence 5073 BP; 1280 A; 1390 C; 1347 G; 1056 T; 0 other:

Query Match 33.6%; Score 1268.2; DB 21; Length 5073;
Best Local Similarity 63.6%; Pred. No. 1.2e-277;
Matches 2015; Conservative 0; Mismatches 1113; Indels 39; Gaps 4;

OY 250 agatacgcctcctcgtgtgaagctctggcctcgtgcttgggtggagataaatacca 309
DB 163 agattcctctggaagaaggaagctatggctgacaccttcgagcgtggaactgtataaca 222
OY 310 ttgctgtgaagtaactcgtgtccagactctgcaagaagaatacaagaagtatggaag 369
DB 223 cgttgaccaaatcctaagctcctctctgtcgtcagaagaagatacagatgtggaatcca 282
OY 370 acgttgcataagaagaatgtatggtcctcacaactgtglaagaagctgcaaaagaacatgg 429
DB 283 gctctgaagatcgaagaagtggtatggtcttgagatggttggaagatctcagaagacatgg 342
OY 430 aagaagatgtttcaacaagaagctgagccgtcagcgctgtggtggaagctgcaagaagaag 489
DB 343 agaacatgtctcggaagaagtcgaagcggtccagaatctgtgtgaagctgcgaggaag 402
OY 490 caaacctgaacatgaattgtatgcagacttcagatgaataacttcaatgtctgtgctta 549
DB 403 ccgacctgaaccaagaatcattgaatccctgtgtgtcgaacttaacactcgtgtcttga 462
OY 550 taatgaagggacaaagaagcgaatttttggagctgggaagaagatcatcatcaggccc 609
DB 463 tcaacgagagggagcagaagggcacaattcgttgagctgtggcgccgagatctccctcggagt 522

QY	610	caatygacattttaaatttgctctgtgaacatcagtlctaagltgacgtccaaatlaccaa	665
Db	523	ccaattctcaattcagcaaacctctgcgtgtgaacacctccatcagaagcgtctcagctccca	582
QY	670	cgaaactgtcaacaagaagccctgcgaattgtcaatgtgaggtttttgtgtcgaattctaa	729
Db	583	ccaacgtgtacaacaagaagcccaagatattttaaattgagatctacatgtctcgaagccttga	642
QY	730	acaaagttttttgtagaataactgtgacacgtgacacatctccatctcgaatgacgtacttggaa	789
Db	643	atgctgtctctgtgaggaactcttcagagagacccaacglttgacctgtgcaattatttggca	702
QY	790	gtcgaaagggtctttttaaagcagltccggggatctaaatvggaaaccegatvgaaatvgag	849
Db	703	gtcgaaactgtattcttcagatctacatcaggtataaattgacaacctgtgagaatvgag	762
QY	850	tcaattgctctgactctcaggaacccgaaatgtgatactccagcgacgtactctccgaag	909
Db	763	tcaattacatttgcactgcgaaacccgagctgtgatactcaagtctgcactctcccaag	822
QY	910	acgtgtcattttagtttgccgtcagctgagcgacatggaagagcccgctgtactatccgga	969
Db	823	acatagtgtatttgtgtgagcgtgtgagcgtgacgtattgaaagggtcgtgagatgtacattgcba	882
QY	970	agcaaacagctcattccatttttggatacacttggggatgtatgacttcttaacaataatg	1029
Db	883	agcacaccctacccaacacacttcttgacacccctggggagatgacttctgttaatactatag	942
QY	1030	cttataatgagagacttcaactatgttgaacacttgcctgtaatvgaaactttgttgcgaagcg	1089
Db	943	cgtacacatgtactacgtcccatctacatcgtgagcctgtttttaaaggatctcctgtccagcg	1002
QY	1090	acagggcaacaagaagagcactcagggagagatcttggaacaacttttcgcaagaagaaatg	1149
Db	1003	accgagacacatcagagagcaatttcaaacactgctgtgttgagaggaattgtatgttccaaggttgc	1062
QY	1150	gaattgtgataatgctctgtgaatgagagccttcaacactctcgaatgtatcttaacacacacg	1209
Db	1063	gggtcgttggaacgaagccctgagaggaagccttccagatctcgaagcgagttccaagagcgca	1122
QY	1210	gacaaggaagtatctgcagtlcagggccatcaatgtctacatactatgtggcggtvgacaact	1269
Db	1123	agcaaggaagcctctgcacaacagccatcatgtctcatcagcgagcgccgctgtgagagact	1182
QY	1270	atgatatacaattttgcaaaaatacaaatgttgccgaatcogaaggtctcicaatttcaataacc	1329
Db	1183	acgaagccggtgttttgagaaggtlaaacctggccgaactgtcaaggtctccagttttccataacc	1242
QY	1330	tcaatgaaagagagagctgtgctgttcagagacatctaaagtgtatgtgcgtctgtgcacaacaag	1389
Db	1243	tcaattgtggagagaagtgctcttctgtgcgcacggcatgaaigtatgttatgtcaacaacaaga	1302
QY	1390	gaatttttaccagatctccacacttgcgtatgtatgtcagaagaaatgtcagtgaatactctc	1449
Db	1303	gctactacacagcagatctcaacgctgtgcggaacccagagaaagcgtgattgaatactctgc	1362
QY	1450	acgtgttgatccggcccaagaatcatcgaaccaaggaatgtatgtgtgtgtgagacggaact	1509
Db	1363	acgtgtgtccagccgcccaatggtctcatcaaccaagcaacgcagacatcatctgtgacagaagcct	1422
QY	1510	acatttacaagcacctc-----gactgtatgatcaaggcccgctccttgatgaacagcttag	1563
Db	1423	acattggaacgaagctccctcagctctgcaggtctcaggtcccgacatgtctcaacacgttgc	1482
QY	1564	ccatgcctgtgtttagttaaagcagacgaaacagatccgaaggtcgaatctctctcggaggtgc	1623
Db	1483	ccatgcacagctcttcacagaagaagaacgaagacgcatcccatctggtcatctctcctgtgtgc	1542
QY	1624	ttgggcacgaatgtcccacgtgaagaagactcttgagaacccatccccaataaagaatttagga	1683
Db	1543	ttgggtccgaatgtggccctcgagagagatctgataagactgtgcgccctgttaagaactgttag	1602
QY	1684	ttcacggttatgaccttctgtcaatcaacaataatgtgtatctctgtcgcgcatcccgaaactca	1743

Db	1603	tgcaagcgtaacgacctctctgaaacccaacaaatggtctacatctctctccatctccgacctcc	1662
Qy	1744	ggctgctcttaacgaagagggaaaaagagaa---ggaaacctactaataagtagctgtgac	1800
Db	1663	ggccccgtacaagaagagggaagaagaactaaaccacaacctaaactcaacgctgtggtatc	17222
Qy	1801	tctctgaggtggaatgggaaagacccgaatgacgctgtctgaaataatgtaatgtaatcgaa	1860
Db	1723	tctccgaagtgtgagttgggaagaccaggctgtatctctctgaaacagcgtatcatataggg	1782
Qy	1861	agaacggggaagtttccatggaagtgtgaagaagacagtvgaaacaaagggaaacgggtttg	1920
Db	1783	aaacaggtacacctctcgatgagtgtgaaggttccgaatggaataaagggaagcgagttcttc	1842
Qy	1921	tgatgacaagaagactactattatcacagacatcaagggtactctctctcaatttaggttgg	1980
Db	1843	tctgtacaacaagactactctctcaacgaaatcaacgacaccccttcagtttggggggg	1902
Qy	1981	cgcttccacagagtcatacgtgggaataattgtctccgaagggaaatgtaaacatcgaagaagggc	2040
Db	1903	tgtctgtcccggggcccacagggaaataacactctctcttgaggaaacagctctgttggaagaagcc	1966
Qy	2041	tgcatagacttagaaacatcccgatgctgtctcttgacagatgaatggttctacgtgcaacatg	2100
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Qy	2101	acctacaacctcgaaacacgcgcacatctgtctgaagtgaagaagcttaagctctacctaagaag	2160
Db	2023	atatgaccccaagacacccgaagaagcttcaacgacagtataaggccaagatccgctctctcaaca	2082
Qy	2161	gcaaaagaaacctctgctccagtgatgataaaagaatttgatccaagaagatcccttttggacgg	2220
Db	2083	ggaagagaccccgacctgtgagtgatgtgaacgaagagctgtgtccgggaagggtgctgtttgacgg	2144
Qy	2221	tgtgtgagtgcccccatctgaaacggtatgtggaaccaacgacctgggcccctcaacaaatctgaaat	2280
Db	2143	tgtgtgaacagcccccatctgaaagacctaactggaacagcgtctgcccctcaacatgctccgaagg	2202
Qy	2281	ctgaaacaagagcgctggaaggtgtgctctctctctgagcactcgacaagggctctctcaaaatcaac	2340
Db	2203	ctgaaacaacgtgtgtggaatagtgctctctctctgagcaccggggctgtgagctctgaaaaagacgt	2262
Qy	2341	tgttgtgtcgggcgctgagacagctcaacacatcagaactctccgaagaagctgtggcgacaagggga	2400
Db	2263	tgttctgtgtggtctccgagaagaagctctccgaacagaagcttctctgaaacctgtgggacggagcca	2322
Qy	2401	acaattttaaagcagacagaacatttccctctctctgtgtaacggaagagcgtgtgagacagattccag	2460
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Qy	2461	ggagctctcgctactactgatacccatctcaacgtgacgtgacagta-----ataaaagcaatg	2514
Db	2383	gcaagcttctgttcttaaacctccgcgtctgggcaaaagaccgaanaaagtgtcggtgtgaacccaatg	2442
Qy	2515	tgtgtgaacgaagatgaaatccaatccacaggtctctctgtaatgaaacgaaatctccctgtgtgacag	2574
Db	2443	tgtgtgaacggaacagacacagcgtgtggtcggtgtgaccggtgaacaaagagagacagccattgtctgag	2502
Qy	2575	ctgtgaagcatctcaatgaaatctgaaacttttcccaaaaggaagatctctgaaactctgacgaacag	2634
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Qy	2635	agctgtgcttccctgtgagtgcaaatagctcccatcaagcctgtatgatagtgagactgtgtaattgtt	2698
Db	2563	agtgtgacacactgtgtgataatgttcgtgacaaagaagcctgtcgaaagacagtgtatctcgagctgt	2622
Qy	2695	acctcatagaaataaagtgaatttatattttgtgtctgaagaactacaacacagactgtgaagact	2754
Db	2623	tctgtcatctgaaacaacacgggtttcaatctctgtctcccaagaaggtctccgagaagacggggaagat	2682
Qy	2755	tttttgtgtgagatcatcgagggagcctgtgatagaaacaatgtgcataacaatggggtctctttaaag	2814

Db 2683 tctctgggggaggtgagtggtctcttgaccaccagctctgcatgaggggtgttcaagcc 2742
QY 2815 gaattaccccttaatactactcaagcagtgtagagccaagaaggaagcagcgatgagcg 2874
Db 2743 aagtgactctatgactctcagcagctgtgcaaacctcaggtacccaccacagcgagc 2802
QY 2875 ccacatgacctctctgagcttaataagctctctctctcagtaataatgacatgagcag 2934
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QY 2935 aactgtctctctctctgagtaataactctgtagctgtgtagcctcagatagcag 2994
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QY 2995 -----ctaaagcccaagaatltgaacacagaccctgagacctt 3030
Db 2923 aggcacaaagtctctcaatctcaatctccacaaacacagaagagaccgctgagacct 2982
QY 3031 gtgatacgaatactcaagcactctctctgagcgacacatcaaggaagactacaggaata 3090
Db 2983 ggcagacagagtaaccctgtctgtctgtaacagcgacatccggagagcgcaagcgatcg 3042
QY 3091 ttgctctgtaagagctgtcccaagctctctgtcatccagcaaatcccaagcagcaacctgt 3150
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QY 3151 tcatgtgtgtgtgtgagcagcagctcctctgtgaaactgtgtggtggtcccaatcaccatgtgcac 3210
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QY 3211 ccaatgaaatcagagataatgaatcccttaagtgtagaagcttaagggcccgagagata 3270
Db 3163 cgacaggaagtaataataatgactctgtgcaaatgtgacccgagatgcgtctcccaagagctcc 3222
QY 3271 gaagggcccaagaatctgtcatgtgctcctcaatctgtagaagagaaatgcaaggagtgtag 3330
Db 3223 ggcggcgacagactcctgcagacgctctcattccagagagagaatgccagagactgcggcg 3282
QY 3331 gtgagccgagctcgaagcccaagcagagctcctctctctctctctctctg 3377
Db 3283 ggcctctggaacactcagctcgcgcgcctcactctctgtctgtg 3329

RESULT 15
AAS17581
ID AAS17581 standard; cDNA: 3228 BP.
XX
AC AAS17581:
XX
DT 26-FEB-2002 (first entry)
XX
DE DNA encoding novel secreted protein #10.
XX
KW Secreted protein; cytosolic; immunosuppressive; vulnereary; vaccine;
KW antiinflammatory; neuroprotective; nephrotoxic; cardiovascular;
KW human; cancer; autoimmune disease; wound healing disorder; infection;
KW hematopoietic disorder; inflammatory disorder; infertility;
KW neurological disease; psychiatric disease; cardiovascular disease;
KW respiratory disease; renal; gastrointestinal; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..3228
FT /tag- a
FT /product= "Human secreted protein"
PN MO200179454-A1.
XX
PD 25-OCT-2001.
XX
PF 11-APR-2001; 2001MO-US11797.
XX

PR 13-APR-2000; 2000US-196603P.
PR 24-APR-2000; 2000US-199417P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
DR WPI; 2002-061975/08.
DR P-PSDB; AAN09869.
XX
PT New secreted proteins or polypeptides, useful for treating e.g. cancer,
PT autoimmune diseases, wound healing disorder, infections, haematopoietic
PT disorders, inflammatory disorders, infertility, cancer
PS
XX
PS Claim 2; Page 41-42; 92pp; English.
XX
CC The invention relates to an isolated novel secreted polypeptide (I) and
CC polynucleotide (II). (I) and (II) are useful for treating cancer,
CC autoimmune diseases, wound healing disorder, infections, haematopoietic
CC disorders, inflammatory disorders, infertility, neurological and
CC psychiatric diseases, cardiovascular diseases, respiratory diseases,
CC renal diseases, or gastrointestinal diseases. These may also be used to
CC treat diseases, abnormalities and disorders caused by abnormal
CC expression, production, function and/or metabolism of the genes, as
CC vaccines for inducing immunological response in a mammal, and in
CC screening methods for detecting the effect of added compounds on the
CC production of mRNA and polypeptide in cells. The polypeptides can be used
CC as immunogens to produce antibodies immunospecific for the polypeptides,
CC and to identify membrane-bound or soluble receptors. The polynucleotides
CC may be used as diagnostic reagents, in chromosome localisation studies,
CC and in tissue expression studies. The present sequence represents the
CC coding sequence of novel human secreted protein #10.
XX
SQ Sequence 3228 BP; 749 A; 897 C; 932 G; 650 T; 0 other;

Query Match 33.6%; Score 1265.6; DB 24; Length 3228;
Best Local Similarity 63.9%; Pred. No. 3.8e-277;
Matches 2002; Conservative 0; Mismatches 1109; Indels 21; Gaps 5;

QY 267 gtgaagctctgggctgctgcttgggtggagataaatcatctgctgcaagtacc 326
Db 61 gtgaagctatggtgacacacttcggcgagctgtataactactgtgacaaatcactca 120
QY 327 ggtccagctctgcgaagaataatacaagaatgtagaagcagctgtccataagaaga 386
Db 121 ggcctctctgctgcgagaaagaatgtagaagcttccagctgaaatcgaagag 180
QY 387 attgatgctctcaactgtgtaagaagctggaagaacatgtagaagatgtttcacaag 446
Db 181 gtgagtgtctggaagctgtgtgtagaagcttccagagagacatgtagaagatctgcgag 240
QY 447 aagctgagggcgctcagggctgtgtgtaggctgcagaagaagacacactgaaatgaa 506
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OM nucleic - nucleic search, using sw model

Run on: August 16, 2002, 16:12:30 ; Search time 125.14 Seconds
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Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	130.6	3.5	3566	1 US-07-745-206A-24	Sequence 24, Appl
2	130.6	3.5	3566	2 US-08-311-363-24	Sequence 24, Appl
3	130.6	3.5	3579	1 US-08-455-543A-36	Sequence 36, Appl
4	130.6	3.5	3579	2 US-08-193-078B-25	Sequence 25, Appl
5	130.6	3.5	3579	2 US-08-223-305C-36	Sequence 36, Appl
6	130.6	3.5	3579	3 US-08-949-386-32	Sequence 32, Appl
7	130.6	3.5	3579	3 US-08-450-562-32	Sequence 32, Appl
8	130.6	3.5	3579	4 US-08-984-709A-32	Sequence 32, Appl
9	130.6	3.5	3600	1 US-08-455-543A-33	Sequence 33, Appl
10	130.6	3.5	3600	1 US-08-455-543A-33	Sequence 33, Appl
11	130.6	3.5	3600	2 US-08-193-078B-11	Sequence 11, Appl
12	130.6	3.5	3600	2 US-08-223-305C-11	Sequence 11, Appl
13	130.6	3.5	3600	2 US-08-223-305C-33	Sequence 33, Appl
14	130.6	3.5	3600	2 US-08-149-097D-11	Sequence 11, Appl
15	130.6	3.5	3600	3 US-08-949-386-11	Sequence 11, Appl
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17	130.6	3.5	3600	4 US-08-984-709A-11	Sequence 11, Appl
18	130.2	3.5	3564	1 US-08-455-543A-35	Sequence 35, Appl
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20	130.2	3.5	3564	2 US-08-223-305C-35	Sequence 35, Appl
21	130.2	3.5	3564	3 US-08-949-386-31	Sequence 31, Appl
22	130.2	3.5	3564	3 US-08-450-562-31	Sequence 31, Appl
23	130.2	3.5	3564	4 US-08-984-709A-31	Sequence 31, Appl
24	130.2	3.5	3585	1 US-08-455-543A-34	Sequence 34, Appl
25	130.2	3.5	3585	2 US-08-193-078B-23	Sequence 23, Appl
26	130.2	3.5	3585	2 US-08-223-305C-34	Sequence 34, Appl
27	130.2	3.5	3585	3 US-08-949-386-30	Sequence 30, Appl

28	130.2	3.5	3585	3 US-08-450-562-30	Sequence 30, Appl
29	130.2	3.5	3585	4 US-08-984-709A-30	Sequence 30, Appl
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31	130.2	3.5	3636	2 US-08-193-078B-22	Sequence 22, Appl
32	130.2	3.5	3636	2 US-08-223-305C-32	Sequence 32, Appl
33	130.2	3.5	3636	2 US-08-949-386-29	Sequence 29, Appl
34	130.2	3.5	3636	3 US-08-450-562-29	Sequence 29, Appl
35	130.2	3.5	3636	4 US-08-984-709A-29	Sequence 29, Appl
36	130.2	3.5	3657	1 US-08-455-543A-20	Sequence 20, Appl
37	130.2	3.5	3657	2 US-08-223-305C-20	Sequence 20, Appl
38	129	3.4	3298	3 US-08-713-118-3	Sequence 3, Appl
39	129	3.4	3298	3 US-09-452-007-3	Sequence 3, Appl
40	128.4	3.4	3802	1 US-08-336-257A-4	Sequence 4, Appl
41	125.2	3.3	3802	1 US-08-404-354B-2	Sequence 2, Appl
42	125.2	3.3	3802	1 US-08-314-083B-2	Sequence 2, Appl
43	125.2	3.3	3802	1 US-08-435-675B-2	Sequence 2, Appl
44	125.2	3.3	3802	3 US-08-884-599-2	Sequence 2, Appl
45	125.2	3.3	3802	6 5386025-7	Patent No. 5386025

ALIGNMENTS

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RESULT 1
US-07-745-206A-24
: Sequence 24, Application US/07745206A
: Patent No. 5429921
:
: GENERAL INFORMATION:
: APPLICANT: Harpold, Michael
: APPLICANT: Ellis, Steven
: APPLICANT: Williams, Mark
: APPLICANT: McCue, Ann
: APPLICANT: Feldman, Daniel
: TITLE OF INVENTION: Human Calcium Channel Compositions and
: TITLE OF INVENTION: Methods
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fitch, Even, Tabin & Flannery
: STREET: 135 S. LaSalle
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60603
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/745,206A
: FILING DATE: 19910815
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Feder, Scott B
: REFERENCE/DOCKET NUMBER: 51504
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-372-7842
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3566 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..3273
:
: US-07-745-206A-24
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: Query Match 3.5%; Score 130.6; DB 1; Length 3566;
: Best Local Similarity 46.4%; Pred. No. 7.2e-22;
: Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;
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; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3273
;
US-08-311-363-24

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RESULT 3
 US-08-455-543A-36
 Sequence 36, Application US/08455543A
 Patent No. 5792846
 General Information:
 APPLICANT: Harpold, Michael
 APPLICANT: Ellis, Steven
 APPLICANT: Williams, Mark
 APPLICANT: Feldman, Daniel
 APPLICANT: McCue, Ann
 APPLICANT: Brenner, Robert
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 METHODS
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92101-2926
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/455,543A
 FILING DATE: May 31, 1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/223,305
 FILING DATE: April 4, 1994
 PRIOR APPLICATION DATA:

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	Best Local Similarity	46.48;	Pred. No. 7.3e-22;		
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RESULT 5
US-08-223-305C-36
Sequence 36, Application US/08223305C
Patent No. 5851824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McGue, Ann
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3579 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 35..3289
OTHER INFORMATION: Standard name "alpha2"
NAME/KEY: 5' UTR
LOCATION: 1..34
OTHER INFORMATION:
NAME/KEY: 3' UTR
LOCATION: 3290..3579
OTHER INFORMATION:
US-08-223-305C-36
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Best Local Similarity 46.4%; Pred. No. 7.3e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;
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RESULT 6

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US-08-949-386-32
: Sequence 32. Application US/08949386
: Patent No. 6090623
: GENERAL INFORMATION:
: APPLICANT: Harpold, Michael
: APPLICANT: Ellis, Steven
: APPLICANT: Williams, Mark
: APPLICANT: Mcclue, Ann
: APPLICANT: Gillespie, Allison
: TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
: TITLE OF INVENTION: METHODS
: NUMBER OF SEQUENCES: 38
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Brown, Martin, Haller & McClain
: STREET: 1660 Union Street
: CITY: San Diego
: STATE: California
: COUNTRY: US
: ZIP: 92101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/949,386
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/290,012
: FILING DATE: 11-AUG-1994
: APPLICATION NUMBER: 08/149,097
: FILING DATE: 5-NOV-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/105,536
: FILING DATE: 11-AUG-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Seidman, Stephanie L.
: REGISTRATION NUMBER: 33,779
: REFERENCE/DOCKET NUMBER: 519808
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 238-0999
: TELEFAX: (619) 238-0062
: INFORMATION FOR SEQ ID NO: 32:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3579 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 35..3289
: OTHER INFORMATION: /standard_name="Alpha-2e"
: FEATURE:
: NAME/KEY: 5'UTR
: LOCATION: 1..34
: FEATURE:
: NAME/KEY: 3'UTR
: LOCATION: 3289..3579
: US-08-949-386-32

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Query Match 3.5%; Score 130.6; DB 3; Length 3579;
Best Local Similarity 46.4%; Pred. No. 7.3e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;
QY 346 agaatcaaaagatagagaagcgttgcacatagaagaatgatggtcctcaactg 405
Db 210 ATATTATGAGAAATATCAAGATTTGTATCTGTGAACCAAAATATATGACAGCGCTGG 269
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; Sequence 32, Application US/08450562
; Patent No. 6096514
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann
; APPLICANT: Gillespie, Allison
; APPLICANT: Feldman, Daniel
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: US
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,562
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/404,950
; FILING DATE: 13-MAR-1995
; APPLICATION NUMBER: 08/356,257
; FILING DATE: 7-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/314,083
; FILING DATE: 28-SEPT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/311,363
; FILING DATE: 23-SEPT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/290,012
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/223,305
; FILING DATE: 4-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/193,078
; FILING DATE: 07-FEB-1994

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      APPLICATION NUMBER: 08/149,097
      FILING DATE: 5-NOV-1993
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 08/105,536
        FILING DATE: 11-AUG-1993
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 07/914,231
        FILING DATE: 13-JULY-1992
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 07/868,354
        FILING DATE: 10-APR-1992
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: PCT/US92/06903
        FILING DATE: 14-AUG-1992
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        FILING DATE: 15-AUG-1991
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        FILING DATE: 08-NOV-1990
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 07/482,384
        FILING DATE: 02-FEB-1990
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: PCT/US89/01408
        FILING DATE: 04-APR-1989
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 07/176,899
        FILING DATE: 04-APR-1988
      ATTORNEY/AGENT INFORMATION:
        NAME: Seidman, Stephanie L.
        REGISTRATION NUMBER: 33,779
        REFERENCE/DOCKET NUMBER: 6362-519812
        TELECOMMUNICATION INFORMATION:
        TELEPHONE: (619) 238-0062
        TELEFAX: (619) 238-0062
        INFORMATION FOR SEQ ID NO: 32:
        SEQUENCE CHARACTERISTICS:
          LENGTH: 3579 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: double
          TOPOLOGY: linear
        MOLECULE TYPE: DNA (genomic)
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          NAME/KEY: CDS
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Query Match      3.5%; Score 130.6; DB 3; Length 3579;
Best Local Similarity 46.4%; Pred. No. 7.3e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

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RESULT 8
US-08-984-709A-32
Sequence 32, Application US/08984709A
Patent No. 6320032
GENERAL INFORMATION:
APPLICANT: Williams, Mark E.
APPLICANT: Stauderman, Kenneth A.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McCaulliffe
STREET: 4250 Executive Square, Suite 700
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,709A
FILING DATE: 02-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 450-8400
TELEFAX: (619) 587-5360
INFORMATION FOR SEQ. ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 3579 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 35..3289
OTHER INFORMATION: /standard_name= "Alpha-2e"
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..34
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LOCATION: 3289..3579
US-08-984-709A-32

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RESULT 9
US-08-455-543A-11
; Sequence 11, Application US/08455543A
; Patent No. 5792846

GENERAL INFORMATION:

APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SRO ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 35..3310
OTHER INFORMATION: /standard_name="Alpha-2"
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..34
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 3308..3600
US-08-455-543A-11

Query Match 3.58; Score 130.6; DB 1; Length 3600;
Best Local Similarity 46.48; Pred. No. 7.3e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

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; Sequence 33, Application US/08455543A
 ; Patent No. 5792846
 ; GENERAL INFORMATION:
 ; APPLICANT: Harpold, Michael
 ; APPLICANT: Ellis, Steven
 ; APPLICANT: Williams, Mark
 ; APPLICANT: Feldman, Daniel
 ; APPLICANT: McCue, Ann
 ; APPLICANT: Brenner, Robert
 ; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 ; TITLE OF INVENTION: METHODS
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/455,543A
 ; FILING DATE: May 31, 1995
 ; APPLICATION NUMBER: 08/223,305
 ; FILING DATE: April 4, 1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/868,354
 ; FILING DATE: April 10, 1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/745,206
 ; FILING DATE: 15-AUG-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/620,250
 ; FILING DATE: 30-NOV-1990
 ; APPLICATION NUMBER: US 07/482,384
 ; FILING DATE: 20-FEB-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/603,751
 ; FILING DATE: 04-APR-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/US89/01408
 ; FILING DATE: 04-APR-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/176,899
 ; FILING DATE: 04-APR-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L.
 ; REGISTRATION NUMBER: 33,779
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619)238-0999
 ; TELEFAX: (619)238-0062
 ; INFORMATION FOR SEQ ID NO: 33:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3600 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 35..3310
 ; OTHER INFORMATION: /standard_name= "Alpha-2b"
 ; FEATURE:
 ; NAME/KEY: 5'UTR
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NAME/KEY: 3/UTR
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US-08-455-543A-33

Query Match 3.5%; Score 130.6; DB 1; Length 3600;
Best Local Similarity 46.4%; Pred. No. 7.3e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

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DB 870 TGTTAGAAACCTCTCAGATGATGATTTCTGTAATGATGATTTTCAACGCAATGCTC 929
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DB 984 TGTGTAAGAGCGGCTGAATTAATACACAGCCAAAGAAATTAACGA:TAATAAGAGGGCT 1043
QY 1168 tgaatgagccttcaacatctgagatgattcaacacacaggaacaaagaatgaaatgaaatg 1227
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DB 1044 TTAGTTTGGCTTTTGAACAGCTGTTAATTAATTAATGTTTCCAGAGCA:-----AACTGCA 1097
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DB 1098 ATTAAGATTATTAATGATTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1157
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QY 1288 aatacaattgcccagatcgaagaagctgcacatcttcaacatacattcatggaagagcgtg 1347
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DB 1158 AATACAT:---AAGATAAAAAACTACGTGATTCAGGTTTTCAGTGTGCTAACACAAATT 1214
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DB 1215 ATGAGAGAGGACCTATTCAGATGATGAGCTGTGAAGCAAGGTTTATTAATTAATTAATTC 1274
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DB 1275 CTTCATTGTTGCAATTAAGATTAATCTCAGGAATATTTGGATGTTTGGGAAGACCAA 1334
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DB 1335 TGTGTTTAGCGAGGACAAAGCTTAAGCAAGTCGAATGACAAATGTGACTGATGATCAT 1394
QY 1522 ctctgactgataatgacagggcccgctcctgatagacacatgacatgacatgactgactg 1581
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DB 1395 TGAAGCTGGGACTGTGCTATTCTGGAACCTTTCGGTCTTCAACATTAACCGCAATTTG 1454
QY 1582 agcagaacgaacacagatcgaaagcattctctcggagatggttgccagatgctccag 1641
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DB 1455 AAAATTAAGACAAACTTAAGAACCAAGCTGATCTTGTGTGATGAGATGATGTGCTT 1514
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DB 1515 TGAAGATTAATTAAGACTGACACACAGCTTTTACACTGTGCCCCAATGGATTAATTTG 1574
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DB 1635 CTCAGAGCCA 1645
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RESULT 11
US-08-193-078B-11
Sequence 11, Application US/08193078B
Patent No. 5846757
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BROWN, MARTIN, HALLER & MCCLAIN
STREET: 1660 UNION STREET
CITY: SAN DIEGO
STATE: CA
COUNTRY: USA
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193.078B
FILING DATE: 07-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/868,354
FILING DATE: 10-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991

ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 35..3310
OTHER INFORMATION: /standard_name="Alpha-2b"
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..34
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 3308..3600
US-08-193-078B-11

Query Match 3.5%; Score 130.6; DB 2; Length 3600;
Best Local Similarity 46.4%; Pred. No. 7.3e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

QY 346 ggaataacaaagatgatagaagaacgctgacataagaagaattgagcctcaactg 405
DB 210 AATTATTAGAAATATCAAGATTGTATCTGTGACCAACCAATTAATGACGACCTG 269
QY 406 taagaagctgcaagaagaacgagaagtcttcaagaagcttgaggccgtaagc 465
DB 270 TGAATTTGACAGCGAGATTTGAGAACTCTGAGCAACAGATTTAAAGCCCTGTGA 329
QY 466 gctcgtctgagagctgcagaagaacacacctgaaacataatgacgca 516
DB 330 GCCTGGCATTGGAGCGGAGAAAGTTCAAGCAGCTCACCAGTGGAGAGAAATTTGCA 389
QY 517 acttaacgatagaataactcaatgcgtgctgataaagaagaagcaagaagcgaatt 576
DB 390 GCAATGAACTGCTCAATGCAATGCAAGATGATCTCATCTCGAGAAAATGACAGTG 449
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DB 450 ACCGAGCGCAGAGAGATAAACCTGTTTCAATTGAGATGCTAATTTTGGACAGCA 509
QY 637 tgaacatcagcttaagtcgaagtcgaagtcgaagtcgaagtcgaagtcgaagtcga 696
DB 510 TATCTTATTCAGCAGCAGCAGCTCAATTCCTACTGACATCTATGAGGGCTCAACAAT 569
QY 697 tctgaatgggggttaattgctgaatcctcaacaagaattcttctagaataacttgacc 756
DB 570 TGTAAATGAACCTCAACTGAGACAGTGCCTTAGATGAATGAAATTAAGAAATCGG 629
QY 757 gtagaccatctctcatalgagcagtaacttggaagtgcaagaagcttctttagcgatc 816
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DB 690 CAGCTTACACCATGGGTGATATATAGTAAGAACCTCAAAATTAAGTTGACCTTTATG 749
QY 868 ggaaccgaataatgacatcgaagcaactctccgaagaagcgtgcatctttagctg 927
DB 750 GCAGAGAGCAATGATGATCAAGAGCTGATCTCTTAAGACATGCTTATTCTGTGG 809
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DB 810 ATGTAGTGGAGAGTGTAGTGTGACTTAACCTGATCCAGAACATCTCTCCGAAA 869
QY 988 ttctgatacactgggagatgactcttcaacataatgcttataagagagctc 1047
DB 870 TGTAGAAACCTCTCAGATGATGATTTCTGATGATGAGTTTCAACGCAATGCTC 929
QY 1048 actatgtgaacacttgcctgaatgaaacttggctgaagcgcgaagcaacaagaagc 1107
DB 930 AGGATGAACCTGTTTCAACACC-----TGTGCCAGCAATGTAAAGAAATAAAG 983
QY 1108 acttcgggagatctggaaacacttctgcgaagaagaattgaaatgctgatatgctc 1167
DB 984 TGTGAAGAGCGCGTGAATTAATCAACAGCAAGAAATTAAGATTAAAGAGCGCT 1043
QY 1168 tgaatgagcctcaacatctgagtgatctcaaccaacggaagaagatctgca 1227
DB 1044 TTAGTTTGTCTTTGAACAGCTCTTAATTAATGTTTCCAGACA-----AACTGCA 1097
QY 1228 gtaagccatcaltgctcaataactgatacggtgagacctaataatgacatcttgcaa 1287
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DB 1158 AATACAAAT--AAAGATAAAGATAGTGTATTCAGGTTTCAAGTTGTCAACACAAT 1214
QY 1348 cgttcgaagaaatcctaagtgatgagcgtgccaagaagaatttlaaccagatc 1407
DB 1215 ATGAGAGAGAGCCTTATTCAGTGTGATGGCTGTGAACAAAGATTATTATTAAGAAAT 1274
QY 1408 caaccttgctgatactgcaaggaatgcaatgaataacttcaacgtctgaagcgccca 1467
DB 1275 CTTCATTTGCTGCATTAAGATCAATCAACGAAATTTGATGTTTGGAGAACCA 1334
QY 1468 aagtcac-----cgaacgaagcatgagtgctgagcggaagctcatatgaaaga 1521
DB 1335 TGTCTTTAGCAGAGACAAAGCTTAACCAAGTCCAAATGACAAATGCTGAGATGAT 1394
QY 1522 ctctgactgatactcagagcccgctcctgatagcacactgtaacatgacgtgctgtagta 1581
DB 1395 TGGAACTGGGACTTGTCTTACTGAAACCTTCCGGTCTTCAACATTAACCGGCAATTTG 1454
QY 1582 agcagaagaacacagatcgaaagcactctctcggagtgctggaagaatgctccag 1641
DB 1455 AAAATTAAGCAAACTTAAGAACCAACCTGATTTCTGTTGATGAGGAGATGCTCT 1514
QY 1642 tgaagaacacttgaagacatcccaataacaaatgaagttaagatctcagcttgccttg 1701
DB 1515 TGGAAATATTAAAGACTGACACAGCTTTTACTGTCGCCCAATGGGATTTACTTTG 1574
QY 1702 caatcaacaataatgtrlatatcctgaacatcgcgaactcaagctgcgtgaagaag 1761
DB 1575 CAATGATCTTAATGCTTATGTTTATTACATCAAAATTTTCAACGAAGAACCCCAAT 1634
QY 1762 gaaaaagcga 1772
DB 1635 CTCAGAGACCA 1645

RESUR 12
US-08-223-305C-11
Sequence 11, Application US/08223305C
Patent No. 5851824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 57

QY 1522 cctctactgataatcagggcccccctcctgatacaccctgtaaccatgctgtgttagta 1581
DB 1395 TCGAAGCTGGAGCTTGTCAATTAAGTCTTCCGGTCTTCAACATAACCGGCAATTTG 1454
QY 1582 agcagagacgaacccgatacgcagggcattcctcctgagatggttgcaagatgctccag 1641
DB 1455 AAAATTAAGCAACTTAAAGAACCAAGCTGATTCTTGCTGATGGAGTGAATGTCCTT 1514
QY 1642 tgaagaactctcgaagaccatccccaatacagaagttagggaattcaaggttagccttg 1701
DB 1515 TCGAAGATTTAAAGACGACACACCTTTTACACTGTGCCCCAATGGGATTAATTTG 1574
QY 1702 caatcaacaataatgataatcctcgaacgacacccgaactcagctcgtctagaagaag 1761
DB 1575 CAATGATCTTAATGTTATGTTTATATCAATCAAAATCTTCAGCCAAAGAACCCCAAT 1634
QY 1762 gaaaaaagcga 1772
DB 1635 CTCAGACGCA 1645

RESULT 13

US-08-223-305C-33

Sequence 33, Application US/08223305C

Patent No. 5851824

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel

APPLICANT: McCue, Ann

APPLICANT: Brenner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESS: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/223.305C

FILING DATE: April 4, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/868,354

FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206

FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/620,250

FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/482,384

FILING DATE: 20-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/603,751

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US89/01408

FILING DATE: 04-APR-1988

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 3600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 35..3310
OTHER INFORMATION: /standard_name="Alpha-2b"
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..34
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 3308..3600
US-08-223-305C-33

Query Match

3.5%; Score 130.6; DB 2; Length 3600;

Best Local Similarity 46.4%; Pred. No. 7.3e-22;

Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

QY 346 agaaatcacaaagatgatgaaagacgttgcatagaagaatltgatgctcccaatg 405
DB 210 ATATTATGAGAAATCAAGATTGTATCTGTGGAACCAATATATGACCGCAGCTGG 269
QY 406 taagaagctgcgaagaacatggaagatgtttccaagaagatcgtgagccgtcagc 465
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DB 570 TCTTAATGAACTCAACTGAGACAGTGCCTTAGATGAAATTTTCAAAAAGATTCGAGG 629
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DB 630 AAGACCCCTTCAATTAATGTCAGGTTTGGCAGTGCCACTGACCTAGCTCATATTATC 689
QY 817 cgggataaattggaacacagaatgagaatgagatcattgacctgcac-----tgca 867
DB 690 CAGCTTCAACATGGGTGTATATAGAGAAACCAAAATTAAGATTGACCTTTATGATGTC 749
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DB 750 GCAGAGACCATGATGATCAATCCAGAGGCTGATCTCTTAAGACATGCTTATTCGTGG 809
QY 928 agtcaatggcagcatgaaagacatcgtctgacatctgcgaagaacacagctcatcca 987
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Best Local Similarity 46.4%; Pred. No. 7.3e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

Oy 346 agaaatataaagaatctgaaagaacgtctgcaataagaagaattgagctcccaactg 405
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 Oy 466 gctcgt-----gtggagcgtcgcaagaagcacacatgaaacatgaatttgatcgag 516
 Db 330 GCCTGCAATTGGAAGCGGAGAAAGTTTCAAGCAAGCTCACCAGTGGAGAGAAATTTTGCA 389
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 Db 510 TATCTTATCAGACGACGACGATCATATTTCTACTGACATCTATGAGGGCTCAACAATTG 569
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 Oy 1228 gtcaagcacaatctgcaataactgagtgaggcggtgagacacacatgataactctgca 1287
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 Oy 1288 aatacaatctgagcagatcgaagaagctcgacatctcaacatcctcattgagcagaagcgctg 1347
 Db 1158 AATCAAT---AAAGATTAATAAAGTACGATGATTCAGGTTTTCAGTGTCAACCAATTT 1214
 Oy 1348 cgttcgagacatctaaagtgtgagcgtctgcaacaaagaatttcttaccagatct 1407

Db 1215 ATGAGAGAGACCTATTCAGTGTGCTGTGAAAAAAGGTTATTTATGAATTC 1274
 Oy 1408 ccaccttgctgagtgctgcaagaaatgcatgaaatcctcaactgctgcttaagccgcca 1467
 Db 1275 CTTCATTGCTGCAATTAAGATCAATACACAGAAATTTTGGATTTTGGAAAGCA 1334
 Oy 1468 aagtc-----cgaaccagaaatgagtggtgtgagccgaagcttacaatgacaga 1521
 Db 1335 TGCTTTTACAGAGACAAAGCTTAACCAAGTCCAAATGCAAAATGTGATCTGATGAT 1394
 Oy 1522 ctctgactgatacagagcccgctcctcctgataccactgtaacacagctggtttagta 1581
 Db 1395 TGGAACTGGACTTGTCTATTCATGAACTCTTCGCTTCAACATACCGGCAATTTG 1454
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 Oy 1642 tgaagaactctgaaagacatcccaataacaaatgaagtgatcaggttctgcttg 1701
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 Oy 1702 caatcaataatgtrtatatctctgacgcatccggaactcaggtcgtgtaagaag 1761
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 Oy 1762 gaaaaagcga 1772
 Db 1635 CTCAGAGGCCA 1645

RESULT 15
 US-08-949-386-11
 Sequence 11, Application US/08949386
 Patent No. 6090623
 GENERAL INFORMATION:
 APPLICANT: Harpold, Michael
 APPLICANT: Ellis, Steven
 APPLICANT: Williams, Mark
 APPLICANT: McGue, Ann
 APPLICANT: Gillespie, Alison
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: California
 COUNTRY: US
 ZIP: 92101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/949,386
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/290,012
 FILING DATE: 11-AUG-1994
 APPLICATION NUMBER: 08/149,097
 FILING DATE: 5-NOV-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/105,536
 FILING DATE: 11-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 519808
 TELECOMMUNICATION INFORMATION:


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/ TELEPHONE: (619) 238-0999
/ TELEFAX: (619) 238-0062
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 3600 base pairs
/   TYPE: nucleic acid
/   STRANDEDNESS: double
/   TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/   NAME/KEY: CDS
/   LOCATION: 35..3310
/ OTHER INFORMATION: /standard_name="Alpha-2"
/ FEATURE:
/   NAME/KEY: 5'UTR
/   LOCATION: 1..34
/ FEATURE:
/   NAME/KEY: 3'UTR
/   LOCATION: 3308..3600
/ US-08-949-386-11

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Query Match      3.5%; Score 130.6; DB 3; Length 3600;
Best Local Similarity 46.4%; Pred. No. 7.3e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

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QY 346 agaaatacaaaaggtatgaaagaagcgttgcataagaagaattgagcctccaactg 405
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Db 210 ATATTTATGGAATATCAAGATTTGTATCTGTGAAACCAATTAAGCAGCCAGCTGG 269
QY 406 taagaagcctgcgaagaacatgaaagaagatgttcacaagaagctcgagccgc 465
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Db 270 TAAATTTGCAAGCAGGAGATTTGAGAAACTTCTGAGCAACAGATCTAAGCCCTG 329
QY 466 gctcgt-----gtgagcctgcgaagaagacacactgaaacatgaaattgagcag 516
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QY 517 acttaagcttgaaacttaacttaactgctgctgataaataagaaggaagaagcggaatt 576
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QY 577 ttctggagcctgcgaagaagcttcactcttagccccaatgacatttaataattgctg 636
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QY 637 tgaacatcagctcgaagtcgaagtcgaagtcgaagtcgaagtcgaagtcgaagtcga 696
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QY 697 ttctcaatggggttattggtctgcaatctcctaacaagaattttgtgataacttgacc 756
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QY 757 gtaaccatctccataatgacttcttgaaagtcgaagtcgaagtcgaagtcgaagtcga 816
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QY 817 cggggaattaaatggaaccagatgagaatgagatcaltgcttcgaagcgaagtcga 867
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QY 868 ggaacggaataatgataatcagcgaagtcgaagtcgaagtcgaagtcgaagtcgaagtc 927
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QY 928 acgtcagtcgacagatgaaagacgtcgtctgactatcggaagcgaacagatcactca 987
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QY 988 ttctgataactctggagtgatgactcttcaacataatgcttcaataatgagagctc 1047
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```

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QY 1048 actatggaaccttgctgcaatggaacttbgctgcaagccgacaggaacaacaagagc 1107
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Db 930 AGGATGTAAGCTGTTTTCAGCACC-----TTGTCCAAAGCAAAATGTAAGAAATTAAG 983
QY 1108 actcaaggaagcaltggaacaacttctgcgaagaagatgagatgtgtgataagctc 1167
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QY 1168 tgaatgagccttcaacatctgagtgatctcaacacaacggaagaagatctgca 1227
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QY 1228 gtcagccatcagctcataactatgattggcggtgagacactatgataactcttgca 1287
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 Job time: 14332 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 16, 2002, 16:02:20 ; Search time 3811.76 Seconds

(without alignments)
13349.088 Million cell updates/sec

Title: US-09-787-657-3
Perfect score: 3770
Sequence: 1 tactatagggcgcgcgcga.....aaaaaaaaaaaaaaaaaa 3770

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estbda:*
2: em_estbhum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_lnv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	813	21.6	966	10	BI753834 603027515
2	784.8	20.8	880	10	BI915864 603184526
3	784.2	20.8	798	10	BG206136 RST25571
4	688.8	18.3	738	9	AV723130
5	647.2	17.2	818	10	BE740459
6	633.4	16.8	801	10	BG213431
7	583.8	15.5	608	9	AV722352
8	561.2	14.9	762	9	AV722352
9	518.4	13.8	799	10	BI736456
10	515	13.7	671	10	BE985092
11	492.4	13.1	711	10	BI736450
12	479.4	12.7	589	10	BF465072
13	458	12.1	505	10	BF924114
14	448.8	11.9	570	9	AI928328
15	447.2	11.9	570	9	AW299346
16	432.4	11.5	843	10	BI732344
17	432.2	11.5	782	10	BG295845

18	431.4	11.4	533	10	BE949415
19	420	11.1	420	9	AI880300
20	419	11.1	422	9	AI188635
21	414.8	11.0	628	10	BM114312
22	405.2	10.7	551	9	AM655372
23	404.4	10.7	502	9	AM491939
24	401.4	10.6	450	9	AI290166
25	392.8	10.4	408	10	BE768630
26	369.6	9.8	509	9	AI190607
27	363.4	9.6	365	10	BE711310
28	361.8	9.6	365	10	BE702896
29	361.8	9.6	365	10	BE702897
30	361.8	9.6	365	10	BE764531
31	361.2	9.6	381	10	BE702863
32	359.2	9.5	364	10	BE943019
33	358.6	9.5	365	10	BI035064
34	356	9.4	462	10	R20288
35	354.2	9.4	421	9	AI624354
36	344	9.1	357	9	AM014849
37	343.4	9.1	357	10	BE768691
38	339	9.0	340	10	Z44942
39	330.6	8.8	428	9	AA815447
40	328.8	8.7	332	10	BE768727
41	328.2	8.7	365	10	BE764499
42	325.8	8.6	390	9	AI051759
43	321.4	8.5	402	10	BE523873
44	317.4	8.4	352	9	AW344398
45	309.6	8.2	393	10	BF364513

ALIGNMENTS

RESULT 1
BI753834 603027515F1 NIH_MGC_114 Homo sapiens CDNA clone IMAGE:5198019 5', LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

666 bp mRNA linear EST 25-SEP-2001
603027515F1 NIH_MGC_114 Homo sapiens CDNA clone IMAGE:5198019 5',
mRNA sequence.
BI753834
BI753834.1 GI:15745412
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 966)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-f@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: L1AM1495 row: n column: 04
High quality sequence stop: 784.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5198019"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
/note="Organ. Brain; Vector: pCMV-SPORT6; Site_1: NotI;
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male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for

FEATURES

source

full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH-MGC Library.

	Query Match	21.6%	Score 813;	DB 10;	Length 966;	
	Best Local Similarity	94.3%	Pred. No. 1.6e-108;			
	Matches	919;	Conservative	0;	Mismatches 47;	Indels 9; Gaps 7;
Oy	2526	agtaacatccatccagctcctcgatgaaaccgaatacttcctgtgtgtgcagctgtaagcaatt	2585			
Db	1	AGTACATCATCCACGACTCCTGGATGAAAGGAATCTCGTGGTGGCAGCTAGGCATT	60			
Oy	2586	cagaatgaacttgaattttccaaggaaagtcttgagatgccaagaagcaatgtgtctcc	2645			
Db	61	CAGATGAACCTGAAATTTTCCAAAGAAGTCTGAGATGCCAGACAGAGTGTCTTCC	120			
Oy	2646	ctggatggcaaatlgctcccatcacgctgtgatgtagagactgtgaatttgttacctaagac	2705			
Db	121	CTGGATGCAAAATGCTCCATCAGCTGTGATGTAGACTGTGAATGTTAACCTCATAC	180			
Oy	2706	aataatgatatattttgtgtgtctggaagaacacacaagaactgtgaacttttvtgtag	2765			
Db	181	AATAATGATTTATTTTTGGTGTCTGMAACAPACACAGACTGGAGACTTTTTTGGTAG	240			
Oy	2766	atcgagagagctgtgtatgaacaaattgtctaacaatgtagctcctttaaagaataacgctt	2825			
Db	241	ATCGAGSAGCTGTGTATACAANAATGCTTAACATGGSGCTCTTTAAAAGATTACCTT	300			
Oy	2826	tatgaatcaccaagccaatgtgtagaagccaagaagaagcagcgaatgycgccatlygctc	2885			
Db	301	TATACTACTCCAAGCATCTGTAGACCACAAAGGAACACAGATGCGCCCATGGCCTC	360			
Oy	2886	ctggatcctttaaagcttccttccttccttcgcgaataaagtatcaagaagaacttgtctg	2945			
Db	361	CTGATCTCTTAAATGCTTCTCTCTCTGCAATAAATGATCATACAGAACTGTCTTGG	420			
Oy	2946	tctcctgtgtgaatttaaactcttcagtttgtgtgtgacatccgaatagaacgactaaagcccag	3005			
Db	421	TTCTCGTGGAATTTAACCTCTGCAGTTGGTGGGCACTCCGATATGACAGCTAAGCCAG	480			
Oy	3006	aaattgaaaacgacctvgagccttgttatctgaataatccaagatttcgtctcgaagcgc	3065			
Db	481	AAATTTGAACAGACCCTTGAGACCTTGATATCTGAATTTCCAGACTTCTCTGAGGCG	540			
Oy	3066	accaatcaagygactacaaggaatatlgctgtgtgaagactgtccaaagctcttgtcatac	3125			
Db	541	ACCATCAAGAGGACTACAGGGGAAT- TGCTTGTGAAGCTCTCCAACTCTTGTCTATC	599			
Oy	3126	cagcaaatcccaagcagcaaacctgtlcaatgtgtgtgtgaagcagcagactgtcctctbgaa	3185			
Db	600	CAGCAAAATCCCMACACAGCACCTGTCTATGTGTGGTGGGACACAGACTGCTCTGTGAA	659			
Oy	3186	tctgttgcccccaatcacacatggaaccccatgtgaataatgaatlaatgtaacttaagtgt	3245			
Db	660	TCATGTGCCCCCATCACCATGGCACCCATTAAATCAAGTATTAATGAATCCCCTTAAGTGT	719			
Oy	3246	gaacgctcaaagsgcccaagaatlcagaagaagcgcacagaatatgtlcalgygctlccalct	3305			
Db	720	GAAAGCTTAAAGG-C- CCAAGATATCAGAAAGGCGCCAGAAATGTGCATTTG-- TTCCATCT	776			
Oy	3306	gagagaagaatcagaagggatgtgtgggggtgtgcgcggatgtlccaaagcccaagcagctcctc	3365			
Db	777	GAGGAGATGKACAGAGCTGTGGGGGTGCGCAGAGTCTCC- AGCCCAACAGTCTTTCCTT	835			
Oy	3366	ctgtctccctcgccttltgatgtcctcttccaaggtgacacatgacatgtatccttact	3425			
Db	836	TCGTGCTCTG- GTTGTATGCTCTTCTCAAGGTGACACTGACAGAAATTTCTCTACT	894			
Oy	3426	gaactgaagcttctctgtgcataatgataatgataactgtgaacccaataatgtgtc	3485			

Db	895	GACTGAATG-TCTCGGGGATGGGTTATCATCG--TAATGTGACAAAAATTTGGGCAC	951
Qy	3486	aactacagacatg	3500
Db	952	TACACACCTGAATG	966

RESULT	2
LOCUS	B1915864
DEFINITION	B1915864 603184526p1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5248447 5', mRNA sequence.
ACCESSION	B1915864
VERSION	B1915864.1 GI:16179807
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 880) NIH-MGC http://mgc.ncl.nih.gov/.
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE	Unpublished (1999)
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: csapbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://llnl.gov Plate: LLAM1627 row: c column: 08
FEATURES	High quality sequence stop: 740. Location/Qualifiers 1..880 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5248447" /clone_11b="NIH_MGC_121" /lab_host="DH10B" /note="Organ: brain; Vector: pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: This is a NIH-MGC Library."
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Query Match	20.8%; Score 784.8; DB 10; Length 880;
Best Local Similarity	96.6%; Pred. No. 2e-104; Indels 2; Gaps 2;
Matches 823; Conservative	0; Mismatches 27;
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Dd 1	ATGGAATCATGACAGAACTTTGTCTTCTCCTGGTGGAATTAACTCTGCAGTTGGCGCA 60
OY 2981	ctccgatatgacagctaaggcccagaagaattgaacaacaccctgtgagcctttgatactga 3040
Dd 61	CTCCGATATGACAGCTAAGCCCAAGAATAATTGAACAAGACCCTGGAGCCCTGTGATACTGA 120
OY 3041	atatccaagcattgcctctcgagcgaccatcaagaagagactacaagggaatatatgctgtga 3100
Dd 121	ATATCCAGCAATTCGCTCTCTGAGCGCACCATCATCAAGAGACTACAGGGAAATATGCTTGTA 180
OY 3101	agaactgcccaagtccttctgtcatcccaagaatcccccaagcaagaaccttcatatggttgtt 3160

QY	Db	181	AGACGCTCCCAAGTCCTTTGGTCATCCACAGAAATCCCAAGCAGCAACCTGTTTCATGCTGTG	240
QY	3161	ggtggacagcagcgtgcctctctgtaactctgtgcccccaatcaaccatgagcaccattgaaat		3220
Db	241	GGTGGACAGCAGACGCTGCTCTGTGAATCTGTGGCCCCCATCACCATTGAGGACCCATTGAAT		300
QY	3221	caagtataatgataatcccttaagtgtgtaacgtcttaaggcccaagaatcagaaggccccc		3280
Db	301	CAGGTATATATGTAATCCCTTAAAGTGTGAACGCTTAAAGGCCCGAAGAATCAGTAAGCGGCC		360
QY	3281	agaactctgtcaatgcttccatccctcgaaggagaatgcaaggagatgtgtaggtgtgccccgag		3340
Db	361	AGAACTCTGTCAATGCTTCCATCTCTGAGAGAAATCAAGGAGGTGTGAGGCGCCCGAG		420
QY	3341	tctccaagcccaagaagaagctcctctctgtgcctcctctgctt-tgaatgctctctcaagt		3399
Db	421	TCTCCAAAGCCCGACAGAGTCCTCTCCATCTCTGAGAGAAATCAAGGAGGTGTGAGGCGCCCGAG		480
QY	3400	gaacatgactgagatgctctctcttactgactgagatgctctctctctgacatgataatcatg		3459
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QY	3580	gtatcatcatccttttactcttgccagatcatgcaaatgtgagattgcccacatgataac		3639
Db	661	GTTATCTATCATCTTTTACTTACTGACCACTGATGCAATATGTGAGTTGCGCATGATTAATC		720
QY	3640	accctctcgaagaatgtaggcacgcgaagtgta-aggcatgtgccctctgcttgaacta		3698
Db	721	ACCTCTCATCAAGAAATGAGACCGAAGTGTGACACAGTGTCCCTTGTGTTGAACCTTA		780
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ACCESSION	BG206136			
VERSION	BG206136.1	GI:13727823		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
	1 (bases 1 to 798)			
	Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,			
	Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J.			
	, Lerner,J., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith			
	, E., Veloso,N., Klika,A., Hess,J., Cothen,K., Lo,K., Offenbacher			
	,J., Dantzig,J. and Ducar,M.			
	Creation of genome-wide protein expression libraries using random			
	activation of gene expression			
	Nat. Biotechnol. 19 (5), 440-445 (2001)			
	21227151			
TITLE	Contact: Scott J. Cain			
JOURNAL	Athersys, Inc.			
MEDLINE	3201 Carnegie Ave, Cleveland, OH 44115, USA			
COMMENT	Tel: 216 431 9900			
	Fax: 216 361 9596			

FEATURES		source	1. 798
Email: scai@ethersys.com		/organism="Homo sapiens"	
High quality sequence stop: 551.		/db_xref="taxon:9606"	
Location/Qualifiers		/clone_lib="Athersys RAGE Library"	
		/cell_line="HT1080"	
		/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."	
BASE COUNT	215 a	196 c	178 g
ORIGIN			209 t
Query Match	20.8%	Score 784.2;	DB 10; Length 798;
Best Local Similarity	99.0%;	Pred. No. 2.5e-104;	
Matches 789;	Conservative	0; Mismatches 8;	Indels 0; Gaps 0;
QY	2822	ccttattgactccaagccatgtgtgtagaccacaagaagcaagcagcagtcgcccattg	2881
DB	1	cccttatgactcaccatgcatgtagaccacaagaagcaagcagcagtcgcccattg	60
QY	2882	cctctctgagctcttaatagccttcctctctgcagttaaatgatacagaaactgt	2941
DB	61	cctctctgagctcttattatagccttctctctccgcagtaaatgatacagaaactgt	120
QY	2942	cttgtctctgtgtgaatttaacctctgcagttgtgtgcactccgatalacagctaaagc	3001
DB	121	cttgtctctgtgtgaatttaacctctgcagttgtgtgcactccgatalacagctaaagc	180
QY	3002	ccagaataatgaaacagaccctgtgagcctgtgtatactgatatccaagcttcgtctcga	3061
DB	181	ccagaataatgaaacagaccctgtgagcctgtgtatactgatatccaagcttcgtctcga	240
QY	3062	ggcgaccatcaagaggagacacacaggaatactgtgtgaagcctgcctcaagctcctgt	3121
DB	241	ggcgaccatcaagaggagacacacaggaatactgtgtgaagcctgcctcaagctcctgt	300
QY	3122	catccagcaatcccaagcagcaacctgtlca tgg tgtgtgtgagaagaagctgctctg	3181
DB	301	catccagcaatcccaagcagcaacctgtlca tgg tgtgtgtgagaagaagctgctctg	360
QY	3182	tgaatctgtgcccccatcacatcattgaccccatgaaatcaggtatataatgcccttaa	3241
DB	361	tgaatctgtgcccccatcacatcattgaccccatgaaatcaggtatataatgcccttaa	420
QY	3242	gtgtgaagctctaaaggcccagaagaatcagaaggcgcccagaatctgtcatagcttcca	3301
DB	421	gtgtgaagctctaaaggcccagaagaatcagaaggcgcccagaatctgtcatagcttcca	480
QY	3302	tccctgaggaatgtcaaggaggtgtggtggtgtgcgcgaatcccaagcccaagacgtct	3361
DB	481	tccctgaggaatgtcaaggaggtgtggtggtgtgcgcgaatcccaagcccaagacgtct	540
QY	3362	cctctgcctcctctgtcttgaatgcctcttccaagggtgacacgtgagatgctctct	3421
DB	541	cctctgcctcctcctgtcttgaatgcctcttccaagggtgacacgtgagatgctctct	600
QY	3422	tactgactgagatgttctctgttgcaatgcataatcctgtaaacgttgaaaccaaatgt	3481
DB	601	tactgactgagatgttctctgttgcaatgcataatcctgtaaacgttgaaaccaaatgt	660
QY	3482	gtgcacaatcagacagatgaatatagttccaacatcagatctcatcagatctttaaact	3541
DB	661	gtgcacaatcagacagatgaatatagttccaacatcagatctcatcagatctttaaact	720
QY	3542	gtgcgtgatataaactcttaagaatagtgtgacaaaagttatctatcaactcttctaact	3601
DB	721	gtgcgtgatataaactctttaaagaatagtgtgacaaaagttatctatcaactcttctaact	780

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OY 3602 tgcacgcatgcaaatg 3618
|||||
Db 781 TGCCAGTCATGCAATG 797

RESULT 4
AV723130 738 bp mRNA linear EST 16-OCT-2000
LOCUS AV723130 HTB Homo sapiens cDNA clone HTBAPB04 5', mRNA sequence.
DEFINITION AV723130
ACCESSION AV723130.1 GI:10826300
VERSION EST.
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 738)
AUTHORS Gu,Y., Peng,X., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X.,
Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu
,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
Chen,J., Chen,Z. and Han,Z.
Homo sapiens cDNA HTB clones
Unpublished (2000)
TITLE Contact: Zeguang Han
JOURNAL Chinese National Human Genome Center at Shanghai
COMMENT 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(Ext. 45)
Fax: 86-21-50801922
Email: hanzg@hgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1..738
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HTBAPB04"
/clone_lib="HTB"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 196 a 182 c 180 g 180 t

Query Match 18.3%. Score 688.8; DB: 9; Length 738;
Best Local Similarity 97.7%; Pred. NO. 1.7e-90;
Matches 721; Conservative 0; Mismatches 12; Indels 5; Gaps 2;
```

```
Db 301 GGACTTCTGAAAGCTGGCGACAGGAGAAATTTTAAAGCAGCAATTCCTCTCTG 360
OY 2432 gtaccgaagcgcgtgaagcagatcccaaggagctcgtctactcagatccatccagcac 2491
|||||
Db 361 GTACCGAAGAGCGCGCTGACAGATTCACAGGAGCTTCGCTACTGATCCCATTCAGCAC 420
OY 2492 tggaccagtcataaagaacatgtgtgtagcagcaagtagacatccatccagctcctgtatga 2551
|||||
Db 421 TGACACAGCAATTAAGCAATGTGGTGACACCAAGTACATCCATCCACCTCTGGATGA 480
OY 2552 acggaaatcctcgtgtgtgtagcagctgttagcactgaagtagaactgaatttttccaag 2611
|||||
Db 481 ACGGAAATCTCTGTGTGTGGAGCTGTAGGCAATACAGATGAATCTTGTTCCTCAAG 540
OY 2612 gaattctgtagtcgcaagcagacagtgcttcctcctgtagtggaatgtccatcagctg 2671
|||||
Db 541 GATGTTCTTGACTGCCAGACAGAGCTGCTTCCTCGATGGCAAAATGCTCATCAGCTG 600
OY 2672 tgatgtaggagctgtgaattgttaccctcatagacaataatgattatgtgtgtctga 2731
|||||
Db 601 TGATGATGAGACTGTGAATTG-TACCTCATAGACAATAATGATTAATTTGTGTCTGA 659
OY 2732 agactacacagactcgagactttttgtgtagtctgagggagagctgtgatacaaat 2791
|||||
Db 660 AGACTACACAGACTGGAGACTTTTGTGTGATGATCGAAGAGCTGTGATGAAC---T 715
OY 2792 gctaacatgagctcctt 2809
|||||
Db 716 GCTAACATGGGCTCTTT 733

RESULT 5
BE740459 818 bp mRNA linear EST 15-SEP-2000
LOCUS BE740459
DEFINITION 601595508P1 NIH_MGC_9 Homo sapiens cDNA IMAGE:3949657 5',
mRNA sequence.
ACCESSION BE740459
VERSION BE740459.1 GI:10154451
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 818)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMN at: image.liml.gov
Plate: L10CM814 row: 0 column: 02
High quality sequence stop: 774.
location/Qualifiers
1..818
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3949657"
/clone_lib="NIH_MGC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB1; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
adapted into EcoRI/XhoI sites using the following 5'
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

BASE COUNT	244 a	169 c	205 g	200 t
ORIGIN				

Query Match	17.2%	Score 647.2;	DB 10;	Length 818;
Best Local	Similarly	Pred. No. 1.8e-84;		
Matches 794;	Conservative	1;	Mismatches 14;	Intels 79; Gaps 6;

OY	954	cgtcctgactatcgagaaacaaacagtcccatccatttggatacaacttcgggaatgatgc	1013
Db	1	CGTGCAGCTATTCGACAAACAAGACTCTCATCCATTTTGGATACACTTGGGATGATGAC	60
OY	1014	tctctacaataatgctttataataatgaggagcttcacitgttgaaacctgtccgaatgga	1073
Db	61	TTCCTCAACATAAATGCTTATATGAGGAGGCTTCACTATGTGAACCTTGCTGTAATGA	120
OY	1074	acttttgtgcaagccgacagaacaaagaagacccttcaggagagcatcttgacaactt	1133
Db	121	ACTTTGGTGCAAGCCGACAGGACAAACAAGAGCCTTTCAGGAGACATCTGGACAACACTT	180
OY	1134	ttcgcgaaggaaatggaatgtltgatatagctcgaatgaggccttcaaatctttagt	1193
Db	181	TTCCGCCAAGAAGATTTGGATGTGGATATATAGCTCTGGAATGAGGCTTCAACATTTCTGACT	240
OY	1194	gattccaacacacacagygacaaagaaatgtactctgcagtcagccatcatgctcataactgat	1253
Db	241	GATTTCAACCACACAGGGGACAAAGAGATATCTGACGTCAAGGCATCATGCTATTACTGAT	300
OY	1254	ggggcggtgagacacctatgatacaatctttgcaaatatacaattgcccagatctgaaaagt	1313
Db	301	GGGGGGGTGGACACTTAATGATATCAATCTTTGGAAAATCAATTTGGCCAGATCGAAAGGTT	360
OY	1314	cgcaccttcacatacctcatcttgagacagagagcgtgcttgcagaaactctaagtggatg	1373
Db	361	CGCATCTTCACATACCTTATTTGGACGAGAGGCTGGCTTTGCGACAAATCTTAAGTGGATG	420
OY	1374	gcctlgtgccaaacaaagatlttttaaccagatctccacctlgtcgtatgtgaggaagaat	1433
Db	421	GCTGTGCCAACAAAGAGATTTTTTTTACCCAAATCTCACCTTGGCTGATGTGCAGAGGAT	480
OY	1434	gtcatggaataaccttcaagctgtcttagccggccccaaagtcatcgcaccggagagcatgattgt	1493
Db	481	GTCATGGAATACCTTCACAGTGTCTTAGCCGG-CCAAAGTATCATGACACAGACATGATGTG	539
OY	1494	gtgtgaccaggaagcttatcatgtaacagacactcgaactgtatgcaggcccccgttcctgattg	1553
Db	540	GTTGTGACCGGAAGCTTAAATTGACAGCACT-----	569
OY	1554	accactgtagccatgctctgtgtttagtaagacagaacacagatctgaaggatctctt	1613
Db	570	-----AGATCGAAGGGCATTTCTT	587
OY	1614	ctggagagtggtttggaacagatgtcccaatlgaagaactcttgaagaaccaatcccaaatatc	1673
Db	588	CTGGAGTGTGTGGCAGCAGATGTTCCACTGAAAGAACTTGTGAAMAACATCCCACAAATAC	647
OY	1674	aagttaggaatcaaggttatgcttcttgcatacaataataatggttatatccctggcgcat	1733
Db	648	AAGTAGGAGGATTCACGGTGTATGCCCTTTGCAATACACAAATATATGATATAT-CTGACGCAT	706
OY	1734	ccggaactcaggtctgtgttacgaagaagaaaaaaacygaaggaanaaccttaactatagtgc	1793
Db	707	CCGGAACCTCAGAGCTCTGTACGAAGAAAAAAGCGAAGGA--(CTAATAATATGTA--	762
OY	1794	gttgaccctctctgagtgatgattggaagaacccgagatlgacgtgtgtga	1841
Db	763	CGTTGACTCTCTGAGAGTGAGTGGGAA-AACGAGATGACGTGTGAAVA	809
RESULT	6		
LOCUS	BG213431	801 bp	mRNA linear EST 21-APR-2001
DEFINITION	RST33037 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.		

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	COMMENT	FEATURES																																	
BC213431	1	GI:13735118	Human.	Human sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothran, K., Lo, K., Offenbacher, J., Danzig, U., and Ducar, M.	Creation of genome-wide protein expression libraries using random activation of gene expression	Nat. Biotechnol. 19 (5), 440-445 (2001)	21227151	Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scaine@thersys.com High quality sequence stop: 477.																																		
FEATURES	source	1. 801	Location/Qualifiers	1. 801	Organization="Homo sapiens"	/db_xref="taxon:9606"	/clone_lib="Athersys RAGE Library"	/cell_line="H11080"	/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is H11080, since a random activation method was used, these sequence tags are not necessarily expressed in H11080 under normal circumstances."	BASE COUNT	221 a 191 c 183 g 205 t 1 others	ORIGIN																																
Query Match	16.8%	Score 633.4	DB 10	Length 801	Best Local Similarity	91.3%	Pred. No. 1.8e-82	Matches 723	Conservative	0	Mismatches 22	Indels 47	Gaps 3																															
2688	aattgttaccatagacataatgattatttggctgtcgaagactcacacagact	2747	13	aattgttaccatagacataatgattatttggctgtcgaagactcacacagact	72	2748	ggaagacttttctgtgtgagatcgagggagctgtgatgaacaattgtcctaacaatggtgtcc	2807	73	ggagaccttttttggtagatcgagggagctgtgatgaacaattgtcctaacaatggtgtcc	132	2808	tttaaaagaattacccttatagtactccaagccatgtgtgaagccaaagaagcagc	2867	133	ttttaaagaaatttaccctttatgactccaagccatgtgtgaagccaaagaagcagc	192	2868	gattgagcccatgagcctctctgtgataccttaatagacctctctcgtcagtaaatgagc	2927	193	gattgagcccatgagcctctctgtgataccttaatagacctctctcgtcagtaaatgagc	252	2928	atgacaagaactgtctgtctgtctcgtgtgataattaaactctcgaagttgtgtgcactcgat	2987	253	atgacagaaactgtctgtctgtctcgtgtgataattaaactctcgaagttgtgtgcactcgat	312	2988	atgacaagctaaagccagagaatttgaacaagacccttgagaccttctgtgatactgaatatcca	3047	313	atgacagctaaagccagagaatttgaacaagacccttgaagaccttctgtgatactgaatatcca	372	3048	gcatcgcgtctcgaagcagccatcaagagagactcaagaggaataatgtctgtgtgaagctgc	3107	373	gcatttcgtctcgaagcagccatcaagagagactcaagaggaataatgtctgtgtgaagctgc	432	3108	tccaagctccttgcataccaagcaaatcccaagcaagaaactgttccatggtggtgtgtgagc	3167

Query Match	15.5%;	Score 583.8;	DB 9;	Length 608;
Best Local Similarity	98.8%;	Pred. No. 2.8e-75;		
Matches 599; Conservative	0;	Mismatches 3;	Indels 4;	Gaps 1

3201 Carnegie Ave., Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atherys.com
High quality sequence stop: 379.

FEATURES	Location/Qualifiers
Source	1..762
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone_lib="Athensys RAGE Library"
	/cell_line="HT1080"
	/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
BASE COUNT	205 a 165 c 186 g 205 t 1 others
ORIGIN	
Query Match	14.9%; Score 561.2; DB 10; Length 762;
Best Local Similarity	89.6%; Pred. No. 5.1e-72;
Matches 682; Conservative 0; Mismatches 69; Infels 10; Gaps 7;	
QY 2635	agtggtctccctgtagtggcaaatgtccatagctgtgtagtgaatgtgaattgt 2694
DB 2	AGTGGTTCCTCGATGAGCGAATCTCCATCAGCTGTGATGATAGACTGTGAATTGTT 61
QY 2695	accatagacaaataatgattattcttgggtgtcgaagacacacagatggagact 2754
DB 62	ACCTATAGACAAATATGATTATTATTTGGTCTCGAAGACTACACATAGATGGAGACT 121
QY 2755	ttttgtgtgagatcgaggagagctgtgtagaacaatgtcaacaatgggtcccttaaa 2814
DB 122	TTTTGTGTGAGATCGAGGAGAGCTGTGATGAAACAAATTGCTAACAATGJGCTCTTTAGAA 181
QY 2815	gaattacccttatactaccacaaagcatggtgtgagagccaagaaggaaacagatggcg 2874
DB 182	GAATTACCTTTATGACTACCAAGCCATGTGTAGAGCCACAAGAAAGAACAGATGGCG 241
QY 2875	cccatggcctccctgtagtcccttaaatgtccctctctctgtcagtaaaatgtagcatgacag 2934
DB 242	CCCATGGCCTCCTGTGATGCTTATATGCTCTTCTCTGACATTAATATGATCATGACAG 301
QY 2935	aactgtgtcttgtctcgtgtggaattaaactctgtgaagtgtgtgacatccgatagacag 2994
DB 302	AACGTGTCTGTCTGTGTGTGGAATTAACCTTGCAAGTTGGTGACATCCGATATGACAG 361
QY 2995	ctaaagccacagaatctgaacaagacccttggagccttgtgatatcgaatccagatctcg 3054
DB 362	CTAAAGCCACAGAAATTTGAACAGACCCGTGGAGCCTTGTGATCTGAATATCCAGCATTTGG 421
QY 3055	tctctgagcgcacatcaagaagagactcaaggaaatattgtctgtgaaagatcgtctccaagt 3114
DB 422	TTTTGAGACGCGCCATCAAGAGAGACTCAAGGATTTTGTGTGAANANCTGTGTCAACT 481
QY 3115	ccttgtgatatccagaagaatcccaagcagaacactgttca-tgtgtgtgtgtgaagcagc 3173
DB 482	CCTTTGTGATGACAGCAAAATCCCAAGCAGACACTGTTCATGTGTGTGAGAGACAGCAAC 541
QY 3174	-tgcctctgtgaatctgtgtgtcccat--caccaatggacaccatgtgaatcaagtataa 3229
DB 542	TTGCTCTGTGGGAATCTGTGGCCCATTCATCCCAATGGCCCATTTGGAAATCAGGTTTAA 601
QY 3230	tgaatcccttaagt--gtgaagctctaaagcccaagaagatcaagaagggccc-agaatc 3286
DB 602	TGGAATCCCTTAATGTGGGAACGTCCAAAAGGCCAAAAGAAACAGAAAGGCGCCGAGAAAT 661
QY 3287	ttgtcat-tgcttccatcctgagagaaatgcagaagagtggtgtgggtgtgcgcagatctcc 3345
DB 662	TTGTCTTGAGGCTTCACTTCTGTGAAGAAATTTGCAAGAGATGTGTGTGATGAGATTCATA 721
QY 3346	a-agccacagacagtcctcctctgtcctcctctgtcttggat 3385
DB 722	AGAGCCAAAAGGCTACTTTCGTGCTCTCTTGGGTGGTTGAT 762

RESULT	9
B1736456	
LOCUS	B1736456 799 bp mRNA linear EST 20-SEP-2001
DEFINITION	603359493r1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5366518 ,
ACCESSION	B1736456
VERSION	B1736456.1 GI:15713469
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 799) NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs.r@email.nih.gov Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LLM11932 row: j column: 23 High quality sequence stop: 793. Location/Qualifiers 1..799 /organism="Mus musculus" /db_xref="taxon:10090" /clone="IMAGE:5366518" /clone_lib="NIH_MGC_94" /tissue_type="retina" /lab_host="DH10B (phage-resistant)" /note="Organ: eye; Vector: pCMV-SPORT6; Site.1: NOTI; Site.2: SalI; Cloned unidirectionally; oligo-dr primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: This is a NIH-MGC library."
BASE COUNT	191 a 211 c 187 g 210 t
ORIGIN	
Query Match	13.8%; Score 518.4; DB 10; Length 799;
Best Local Similarity	86.4%; Pred. NO. 8e-66;
Matches 584; Conservative	0; Mismatches 91; Indels 1; Gaps 1;
QY	2736 tacacacagactgtgagactcttttggtgagatcgaggagtcgtgatgaacaattgcta 2795
DB	116 TCCCTAAGACACTGAGAGATTTTGTGGTAGGTAAGAAGCGTCGTCAACAATTGTGA 175
QY	2796 acaatggctctctttaaaagaattaccctttatlgactaccaagccatgtgttagccaac 2855
DB	176 ACAATGGGCTTCCTTAAAAAGAAATAACCTTGTCGACTACCAAGCCATGTGTAGGCCAAC 235
QY	2856 aaggaagaagcatgtggcgcccataggccctctgtgaccttatatgacctctctctga 2915
DB	236 AAGGAGAGCAGTGCACAGTCCCATGATCTTCTGGACCCCTATAAAGCCCTTCTCTCGA 295
QY	2916 gtaaaaatgatcatgacagaaacttgtctgtctctgtgtgaaatttaacctgcagttag 2975
DB	296 GCCAAGTGATGATATGACGGAACCTGTCTTGTTCCTGTGTGAGATTTAACCTGTGACAGTTGG 355
QY	2976 ttggcatctcgatatgaacagctaaagccccgaatattgaaaacagacctgtgagccttgat 3035
DB	356 TGCGACTCCGAATGACACACTAAAGCCCAGAACTGAAAACAACACCCTGAACTTGTGAT 415
QY	3036 actgatatcacgaacttgtctctgtgagcgacacccaatcaaaagagagactacaaggatatgct 3095
DB	416 ACTGAAATACCCAGCTCTTGTCTTCTGTAGCGACACCAATCCAGAAACCAAGGAAACATTCGT 475
QY	3096 tgtgaagaatgtctccaagtcctttgtlcatcacgaacaatcccaagcagaacctgttcatg 3155

[illegible]

RESULT	10
BE985092	
LOCUS	BE985092
DEFINITION	BE985092 671 bp mRNA linear EST 05-OCT-2000
	UI-M-CG0p-bdh-c-10-0-UI.s1 NIH_BMAP_Ret4_s2 Mus musculus cDNA clone
	UI-M-CG0p-bdh-c-10-0-UI 3', mRNA sequence.

VERSION	BE985092.1	GI:10658046
KEYWORDS	EST	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE	1 (bases 1 to 671)
AUTHORS	Bonaldi,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
MEDLINE	9704447
COMMENT	Contact: Chiu, H

Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: MEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA library preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
The following repetitive elements were found in this cDNA sequence:
3-35, >(CCG)nSimple_repeat
Seq primer: M13 Forward
POLYA-NO.

```
FEATURES      Location/Qualifiers
source        1..671
```

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-CG0P-bdh-c-10-0-UI"
/clone_1fb="N1H.BMAP.Ret4.S2"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pT713D-Pac (Pharmacia) with a modified
polylinker: Site_1: Not I; Site_2: Eco RI; The
N1H.BMAP.Ret4.S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description

```

of the library from which this clone was derived, please visit our web site at brainest.eng.ujow.edu .				
TAG_SEQ=None found"				
BASE COUNT	160 a	164 c	152 t	1 others
ORIGIN	,			
Query Match	13.7%	Score 515;	DB 10;	Length 671;
Best Local Similarity	87.8%;	Pred. No. 2,6e-65;		
Matches 599;	Conservative	0;	Mismatches 71;	Indels 12; Gaps 3;

[illegible]

RESULT	11
LOCUS	B1736450
DEFINITION	711 bp mRNA linear EST 20-SEP-2001 603335948BF1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5365516 5' , mRNA sequence.
ACCESSION	B1736450
VERSION	B1736450.1 GI:15713463
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 711)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: L1M11932 row: j column: 21
 High quality sequence stop: 709.

FEATURES

Location/Qualifiers

1..711
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone_1fb="536516"
 /clone_1fb="NIH_MGC_94"
 /tissue_type="retina"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 3.3 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH-MGC library."

BASE COUNT 178 a 185 c 162 g 186 t

ORIGIN

Query Match 13.1%; Score 492.4; DB 10; Length 711;
 Best Local Similarity 89.0%; Pred. No. 4.8e-62;
 Matches 552; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

2736 taacacagactgagagacttttggtagatgagagagctgtatgaacaattgcta 2795
 114 TCCCTACAGACGTGAGATTTTGGTAGAGTGAAGAGCTGTCATGAACTGTTA 173
 2796 acaatggctctttaaagaattacccttatactgaaccatgtgtagaacca 2855
 174 ACATGGGTCTTTAAATAAATAACCTGTAGACCAAGCCATGTAGAGCCAAC 233
 2856 aaggaagcagagatgagcccatgagcctcttgatccctataatgctcctcga 2915
 234 AAGGAGAGCAGTACAGTCCATGACCTGTGACCCCTATAAGCTTTCTCTGCA 293
 2916 gtaaaatgatacagacagactgtctgtcctgtgtgaatttaacctctgagttg 2975
 294 GCCAAGTGAATATGACGAGAACTGTCTTCTGCTGAGTTTAACTGTGAGTTG 353
 2976 tggactccgatatgaacagctaaagaagaattgaacagaccctggagcctgtgat 3035
 354 TGCACTCCGACATGACAGCTAAAGCCAGAACTGAACACCCGGAACCTTGAT 413
 3036 acggaatcccaactgctgtctgtgagcagacataagaagactatagggaattgct 3095
 414 ACTGAATACCCAGCTTTGTTCTGAACGACCATCAAGAGACCAAGGAAACATTGCT 473
 3096 tgtgaagactgctcaagctctgtcatcacaagaatcccaagcacaacccgttcattg 3155
 474 TGGGAAGAGCTGCTCAAGTCTTCGTATCCACAAATCCGAGTATCAATCTGTCATG 533
 3156 gtgggtgtgagacagagctgctctgtgaattgtgtgcccacatcagatggaaccatt 3215
 534 GTGGTGTGAGACAGTGTCTGTGAGTCCGTGCTCTCTTAACCATGAGCCCATTT 593
 3216 gaataaggtataatgaatcccttaagtgtgaagcgtctaaagcccggaagatcagaag 3275
 594 GAATATGAGGTATATGATCCCTTAAGTGAAGCGTTAAAGCTGCAAGATCAGACGA 653
 3276 cggccgaatctgtcatggtctccatccgagaggaatgcaaggggtgtg99gtg 3333

Db 654 CGTCCAGAAATCTGCAAGGTTTCCATCCTGAGAGATGCAAGAGATGTGGGGTG 711

RESULT 12

BF45072

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

CONTACT: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: msb@mail.nih.gov

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A

tail. The sequence tag present in the cDNA between the NotI site

and the oligo-dT track served to identify it as a clone from the

retina tissue cDNA Library Preparation. M.B. Soares Lab Clone

distribution: Researchers may obtain BMAP cDNA clones from RESEARCH

GENETICS. It should be noted that Bento Soares is generating a

small number of additional specialized non-redundant arrays of BMAP

cDNAs whose availability will be considered under appropriate and

limited collaborative arrangements

Seq primer: M13 forward

POLYA=Yes.

Location/Qualifiers

1..589

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UI-M-CG0p-bdg-d-09-0-UI"

/clone_1fb="NIH_BMAP_Ret4_S2"

/lab_host="DH10B (Life Technologies)"

/note="Vector: p773D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; The

NIH_BMAP_Ret4_S2 library is a subcloned library,

ultimately derived from mouse retina tissue libraries at

various stages of development. For a detailed description

of the library from which this clone was derived, please

visit our web site at brainest.eng.uiowa.edu.

TAG_L1B=NIH_BMAP_Ret4_S2

TAG_TISSUE=adult-retina

TAG_SEQ=GTCCAGCGCCGAC

BASE COUNT 156 a 134 c 147 g 152 t

ORIGIN

Query Match 12.7%; Score 479.4; DB 10; Length 589;
 Best Local Similarity 89.4%; Pred. No. 3.8e-60;
 Matches 516; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

2754 ttttggtagatcgaggagctgtatgataaattgccaataatggctctttaa 2813
 13 TTTTGTGTGAGGTGAAGAGCTGTCTATGAACAAGTTGTTAAACATGCGTTCTTAA 72
 2814 agaattcccttctacaaagccatgtgtagagccaaagaaagcagcatgac 2873

Db	73	AGAAATTAACCTTGGACAGACTAACCAAGCCATGTGTAGAGGCCAACAGGAGAGCACTGACACT	132
Qy	2874	gcccaatggccctccctggaacccttaataatgccttcctctctcgagtaaaatgaaatcatgaca	2933
Db	133	GGCCATGAGCACTTCTGGAGACCCCTAATTAAGGGCTTCTCTCTGCACCCAAAGGATTAATGAC	192
Qy	2934	gaactgtactctgtccctgggtgaaatttaaacctctgcactgtgtgtgaaactccgaatagaca	2993
Db	193	GAACTTGTCTTGTTCCTGGTGGAGTTTAACTGTGCAGTTGGTGGCAGTCCGACATGACA	252
Qy	2994	gctaaagcccgaaattgaacaacagacccttggagccttgtatcatcgaatatccagcact	3053
Db	253	GCTAAAGCCCAAAACTGGAACAGACCCCTGGAACTTGTGATCTGAATTAACCAAGCCTTT	312
Qy	3054	gctctggagcgacacatcaagagagactaagaagaaattgctgtgaaactgtctccaa	3113
Db	313	GTTTCTGAAGCGACCATTCAGAGGAGACCAAGGGAACATTGCTTGCCAAAGTCTGCTCAAG	372
Qy	3114	tcccttgtgataccaggaataatcccaagcagcaacctgttcatctgtgtgtgtgtgacagcagc	3173
Db	373	TCTTTCGTGTCATCCAGCAAAATCCCGAGTACCAATCTGTATCATGGTGTGGTGACACTAGC	432
Qy	3174	tgcacctgtgaaatctgtgtggcccccacatcacatagagacccaattgaaatccgtataatgaa	3233
Db	433	TCTCTCTGTGAATCCGTGTGCTCTCTATTAACCAATGAGCACCATTAATGAATTCAGGTAAATGA	492
Qy	3234	tcccttaagtgatgaacgttctaaaggcccaagaagatcaagaagcgcccaaaatctgtcat	3293
Db	493	TTCCTTAAAGTGTGAACGGTTAAAGGCTCAGAGATCATGACGAGCGTCCAAATCTGCGAC	552
Qy	3294	ggctccatccctgagaggaatgcaagggagtgctgggg	3330
Db	553	GGCTTTCATCCTGAGGAGAGATGCAAGAGAGTGTGGGG	589

RESULT	13
LOCUS	BF924114
DEFINITION	BF924114 505 bp mRNA linear EST 19-JAN-2001
ACCESSION	MR_0701042-271100-101-f08 NT0142 Homo sapiens CDNA, mRNA sequence.
VERSION	BF924114
KEYWORDS	BF924114..1 GI:12320002
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eumetazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
	1 (bases 1 to 505)
	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordini, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsumura, A., Bais, G. S., Simpson, D. H., Brunslein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202653
COMMENT	Contact: Simpson A.J.G.

LUDWIG Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: aslmpson@ludwig.org.br
 This sequence was derived from the FAPESP/ICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR46t2-MR4-NT0142>
 271100-101-f08a6t3-2000-11-27a6t4-1)
 Seq primer: puc 18 forward
 High quality sequence start: 31
 High quality sequence stop: 505.
 Location/Qualifiers

	source	1..505	/organism="Homo sapiens"	
		/db_xref="taxon:9606"		
		/clone_lib="MT0142"		
		/dev_stage="Adult"		
		/note="Organ: nervous_tumor; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."		
	BASE COUNT	142 a	110 c	123 g 127 t 3 others
	ORIGIN			
	Query Match	12.1%	Score 458;	DB 10; Length 505;
	Best Local Similarity	96.3%;	Pred. No. 4.9e-57;	
	Matches 467; Conservative	0;	Mismatches 18;	Indels 0; Gaps 0;
OY	2359 agctaccacatagacttcctcgtaaagctcygggacaagaagacattttaaaggagacc	2418		
Db	10 acctcacatcagcgactgcctgaagacctggcgcaagagagacacatttttaacgcgagacc	69		
OY	2419 attcccccctctgtgaccgaagaagccgcctgtagacatgccaaaggagcttcgtctactcga	2478		
Db	70 attttccctctcgtgtgacggaagagccgcctgacacatttcacagagacgttcgtctactcga	129		
OY	2479 tcccatltaagcactgagccagcaatlaaagaacatgtygtgacagacaatatcatccatcc	2538		
Db	130 ttcccatTTTCAGCACTGTGACAGCAGTCAATTAAGAACAATGTGGTGACACACAATTATCATCC	189		
OY	2539 agctccttgtagaaggaatactcctctgrytggagcgcgtgatgacatltaagttaaatctg	2598		
Db	190 agctccttgtagaaggaatactcctctgrytggagcgcgtgatgacatltaagttaaatctg	249		
OY	2599 aaatttcccaaaggaagtlcttgtagctgcacagacagatgtgtctcccccttgatggaat	2658		
Db	250 AATTTTCCAAAGGAAGTTCTGAGACTGCCAGACAGACATGTGCTCTCCCTGGATGSCAAT	309		
OY	2659 gctccatcaagctgtagatgaagactgyaatgtgttacccatagacaataatgatllta	2718		
Db	310 gctccatcagctgtagatgaagactgyaatgtgtgttaccctatagacmataratgatTTTA	369		
OY	2719 ttcttgtctcgaagactacacacagactggagactttcttgtagatgcgaaggagctg	2778		
Db	370 TTTNGTGTCTCGAAGACTACACACAGACTGNAGACTTTTTGGTAGATCCAGGGAGCTG	429		
OY	2779 tgatgaacaatctgctaacaatlyggctcctttaaagaataaccctltatgactaacga	2838		
Db	430 TGATGACAAATAATGTGCTACATATGGGCTCTTTAAAAGAAATACCCTTATGATCACCAAG	489		
OY	2839 ccattg 2843			
Db	490 ACAAG 494			

RESULT	14			
LOCUS	AI928328/c			
DEFINITION	AI928328	570 bp	mRNA	linear
ACCESSION	U09664.1	NCI-CGAP_Kid1	Homo sapiens	cdna clone
VERSION	AI928328			IMAGE:2463150 3'
KEYWORDS	AI928328.1	GI:5664292		
SOURCE	EST.			
ORGANISM	human.			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
	1 (bases 1 to 570)			
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .			
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
	Tumor Gene Index			

JOURNAL
COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: c9apb@s-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/dbp/Image/Image.html
Insert length: 2253 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 451.

Oy 3603 gccagtcacgcaaalgtgagtltgccaca lgaatacaccccttcacacagaatgggaccg 3662
|||||
Db 152 gccagtcacgcaaalgtgagtltgccaca lgaatacaccccttcacacagaatgggaccg 93
Oy 3663 caagtggttaggcaagtgccctcctcgtctgaaacctatgaaaccaaattaaactgta 3722
|||||
Db 92 caagtggttaggcaagtgccctcctcgtctgaaacctatgaaaccaaattaaactgta 33
Oy 3723 cttctaaataagtcataattaaacataaaa 3754
|||||
Db 32 cttctaaataagtcataattaaacataaaa 1

Search completed: August 16, 2002, 18:17:01
Job time: 8081 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM protein - protein search, using sw model

Run on: August 16, 2002, 20:10:25 ; Search time "6.46 Seconds
(without alignments)
1576.185 Million cell updates/sec

Title: US-09-787-657-5

Perfect score: 5667

Sequence: 1 MAGPGSPRRASRCASALAA.....SLQAGTYVLLPLLMFSR 1085

Scoring table:

BLOSUM62
Gapex 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_032802:*

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*

2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*

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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5667	100.0	1085	21	AA92320
2	5667	100.0	1085	22	AAU01024
3	5667	100.0	1085	22	AAB62248
4	5577	98.4	1065	22	AAU01019
5	5564	98.2	1071	22	AAB62243
6	5459	96.3	1077	22	AAU01026
7	5459	96.3	1077	22	AAB62250
8	5422	95.7	1038	22	AAU01018
9	5422	95.7	1038	22	AAB62242
10	5324	93.9	1019	22	AAU01017
11	5324	93.9	1019	22	AAB62241

12	3515	62.0	1120	21	AA92321	Human alpha-2-delt
13	3482.5	61.5	1097	22	AAU01038	Human secreted sol
14	3482.5	61.5	1097	22	AAB62262	Human calcium chan
15	3417	60.3	1096	21	AA92324	Human alpha-2-delt
16	3365	59.4	1069	22	AAU01037	Human secreted sol
17	3365	59.4	1069	22	AAB62261	Human calcium chan
18	3317	58.5	1050	22	AAU01036	Human secreted sol
19	3317	58.5	1050	22	AAB62260	Human calcium chan
20	3123	55.1	1096	21	AA92323	Human alpha-2-delt
21	2585	45.6	519	21	AA970460	Human membrane cha
22	1520	26.8	1215	21	AAE02340	D. melanogaster cha
23	1394.5	24.6	2172	22	ABB67958	Drosophila melanog
24	1382.5	24.4	1022	22	ABB67234	Drosophila melanog
25	1376.5	24.3	1191	22	ABB60775	Drosophila melanog
26	1200	21.2	1145	21	AA92322	Human alpha-2-delt
27	1200	21.2	1145	22	AAU01023	Human secreted sol
28	1200	21.2	1145	22	AAB62247	Human calcium chan
29	1182.5	20.9	1109	22	AAU01016	Human secreted sol
30	1182.5	20.9	1109	22	AAB62240	Human calcium chan
31	1182.5	20.9	1115	22	AAU01025	Human wild type al
32	1182.5	20.9	1115	22	AAB62249	Human calcium chan
33	1154	20.4	1082	22	AAU01015	Human secreted sol
34	1154	20.4	1082	22	AAB62239	Human calcium chan
35	1153.5	20.4	1106	16	AA973056	Rabbit skeletal ca
36	1151.5	20.3	1091	22	AAU01027	Pig secreted solub
37	1151.5	20.3	1091	22	AAB62251	Porcine calcium ch
38	1148.5	20.3	1106	18	AA937712	Rabbit skeletal ca
39	1148.5	20.3	1106	18	AA918589	Rabbit calcium cha
40	1148.5	20.3	1106	21	AA977545	Rabbit skeletal ca
41	1147.5	20.2	1062	22	AAU01014	Human secreted sol
42	1147.5	20.2	1062	22	AAB62238	Human calcium chan
43	1143.5	20.2	1063	22	AAU01030	Pig secreted solub
44	1143.5	20.2	1063	22	AAB62254	Porcine calcium ch
45	1143.5	20.2	1069	22	AAU01031	Pig secreted solub

ALIGNMENTS

RESULT 1

AA92320

AA92320 standard; Protein; 1085 AA.

XX

AA92320;

AC

XX

10-AUG-2000 (first entry)

DT

XX

Human alpha-2-delta-C calcium channel subunit polypeptide.

DE

XX

alpha-2-delta-C; calcium channel subunit; 3p21.1; gabapentin; cyrostatic;
anticonvulsant; antimigraine; antiparkinsonian; antidepressant.

KW

XX

Homo sapiens.

OS

XX

MO200020450-A2.

PN

XX

13-APR-2000.

PD

XX

07-OCT-1999; 99WO-US23519.

PF

XX

07-OCT-1998; 98US-0103322.

PR

XX

30-OCT-1998; 98US-0106473.

PR

XX

29-DEC-1998; 98US-0114088.

PA

XX

(WARN) WARNER LAMBERT CO.

PI

XX

Johns MA, Moldover B, Offord JD;

PT

XX

WPI: 2000-303744/26.

PT

XX

N-PSDB; AAA09253.

PT

XX

New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
proteins, useful in the treatment of epilepsy, migraine, chronic pain,

	anxiety, multiple sclerosis or cancer
P5	Claim 8; Page 66; 88bp; English.
XX	
RS	The alpha-2-delta-C gene encodes a calcium channel subunit polypeptide.
CC	The gene has been mapped to chromosome 3p21.1. This gene and the related
CC	alpha-2-delta-D and -B genes are useful for protecting mammalian cells
CC	from abnormal calcium flux by introducing expression vectors containing
CC	the respective gene into mammalian cells. The antisense genes are also
CC	useful for treating or preventing epilepsy. The alpha-delta 2 A protein
CC	is a high-affinity binding target of the anti-convulsant drug gabapentin.
CC	Therefore, alpha-delta 2 proteins may also be targeted to treat
CC	seizure-related syndromes, migraine, ataxia, vesibular defects, chronic
CC	pain, sleep interference, anxiety, amyotrophic lateral sclerosis (ALS),
CC	multiple sclerosis, mania, tremor, parkinsonism, substance abuse or
CC	addiction syndromes, mood, depression or cancer.
XX	
SQ	Sequence 1085 AA:
	Query Match 100.0%; Score 5667; DB 21; Length 1085;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 1085; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY	1 MAGPSRRASGASALLAALLVAALGDVNSEDQIPLSVKLMASAFGEIKSIATKY 60
Dd	1 magpsrrasgasaallaallvaalgdvrseqqirplsvklwasafgsktsaaky 60
OY	61 SSSOLLOKKRYKEKDVAIEETDGIQLVKKLKNNEEMHKSEAVRILEAEAHILKH 120
Dd	61 ssgqlkkrykkyekedvaeieidgiqlvyklaknneemhkksaeavrrileaaeahilh 120
OY	121 EFDADLOVEYFNAVLINERDKDNFLLELGEFTLAPNDFNNMLPVNISLSDVQPFPNMYN 180
Dd	121 efdadlgyeyfnavlineredkgnflelgkeftlapndfnlnpnislstdvqyptmyn 180
OY	181 KDPALVNGVYWSLANKVFVNDFNDPDSLIMQIFGSAGCFPPQYRGICKWPEDEGYIADF 240
Dd	181 kdpalvngvwseslnkvfvdnfdndpsllmqifgsagcfppqykwpdepgviadf 240
OY	241 CNRMKVIOAAITSPDDVALVDVSGSMKGRLTIKQVYSILDPTIGDDDFNITAYNEE 300
Dd	241 cnrmkvioaatspddvalvdvsgsmkgrltikqvysildptigdddfnitaynee 300
OY	301 LHYEPCLNGTLVQADRNTKEHFREHLDLFAKGIQMIDLALNEAFNILSDFNHTGGGSI 360
Dd	301 lhyepc lngtlvgadrntkenfhrehldlfakigimidlalneafnilsdfnhtcggsi 360
OY	361 CSQAIMLTLDGVDPDYDTIFAAYNNPDQRVRTEFTLIGEAEAFANIKMKACANGPFPO 420
Dd	361 csqa mltldgvadydtifaaynpdqrvrtfetyligeaeafanikmkacangpfpq 420
OY	421 ISTLADVONENWEYLHVLSRPKVIOEHDDVWTETAYIDSTLTDODGPVLMTVAMPVESK 480
Dd	421 istladvenwemylhvlsrpkvioehddvwttetayidstltdodgpvlmttvampvesk 480
OY	481 ONETRSKGILLGVGTDPVAKELATTIRKYGICHTGVAFATNNNGYILTLPRLRLYEBC 540
Dd	481 qnetrskgilllgvgtdvpvake lktlrpykighcvafatnnngyiltlpelrillyeeg 540
OY	541 KKRKPENKSYVDLSEVEDRDVDLRNMAVMNKGRKFSEMEVKVTYDGKRVLYMINDYY 600
Dd	541 kkrkpensyvdlsevedrdvd lrnmavmnkgrkfsemevkvt ydgk rylvmindyy 600
OY	601 TDIKTPESLGAVALSRGHGKYFFRGNAVTTIEGLHMLEHPDVDSLADEWSYCNTDLPHERRH 660
Dd	601 tdi ktpeslga valsrghgkyffrgnavt tieglhm lehp dvdslade wscntdlpherrh 660
OY	661 LSQLEAIKLYLKGRPELLQCKELIQEVLQFLPAVVVASPIEA VYTSIALKSKSEMDKGVETA 720
Dd	661 lsqleaiklylkgrpellqckellqe vllqflpa vvvaspiea vy tsialk sksemdk gveeta 720
OY	721 FLGRTGTGSRNLTFPGAEQOLTNPDELKAGDKENIPNACHFP LMYRRRAEQIPGSEVYSIP 780

[illegible]

CC voltage dependent calcium channel (VDCC) complexes present in neuronal
CC and non-neuronal tissues including heart and skeletal muscle. Numerous
CC soluble forms of the human calcium channel alpha2delta subunits
CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the
CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are
CC described. The secreted soluble alpha2delta subunit may be used in assays
CC (e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,
CC filter binding or wheat germ lectin flashplate assays to detect or
CC measure the binding or interaction of a ligand (e.g. gabapentin,
CC L-Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine,
CC L-Valine, Spermidine and/or L-Phenylalanine) of a calcium channel
CC alpha2delta subunit.

Query Match	100.0%	Score 5667	DB 22	Length 1085
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1085; Conservative	0	Mismatches	0	Gaps 0

OY	1	MAGPSPRRASGASALLAAALLTAALGDVPSBOIPLSVYKLMASAFGEIKTSIAAXY	60
Dp	1	magspsrrasgasallaaalltaalgdvpsseqipisvsklwesafgeiktsiaaxy	60
OY	61	SGSOLLOKKRYKREKDVAAIEEDIGOLYKLLKMNEMEMHKSSAEVRIVEAAEEAHKH	120
Dp	61	sgsollokkrykrekdvaaiieedigolykllkmmememhksseavriveaaeeahkh	120
OY	121	EFDADLOYEYFAVAILNERDKDGNLELKEKRIIAPNDHFNNLPVNI SLSDVOVPNNMYN	180
Dp	121	efdadloyeyfnavailnerdkdgnflelkekrilapndhfnnlpvnislsvdvpncmyn	180
OY	181	KDPALVNGVYWSESILANKVPVNDPDDPSLIIMQYFGSAKGFPRQYPCJ KNEPDENGIATD	240
Dp	181	kdpalvngvysesilankvvdndpddpsliimqyfgsakgfprqpycknepdenyiatd	240
OY	241	CNNRMFYIOAATSPKDVVTLVDPVSGSMKLRITIAQOTVSLTDDTGDDDFNIITAYNEE	300
Dp	241	cnnrmfyioaatspkdvvtlvdpvsgsmkrlritiaqotvsltdtdgdddfniitaynee	300
OY	301	LHYEPCINGTLVQADRTNKEHFRHLDKLFKAGIGMDIALNEAFNII SDFNHTGOGSI	360
Dp	301	lhyepcingtlvgadrtcnkehfrhldklfakgigm dialneafnii sdfnhtgogsl	360
OY	361	CSQAIMLITDGAQVOTPYDTIFAKYNMPPDRKVRIFETYLIGEAAPADNKKMACANKCFPRQ	420
Dp	361	csqaimliltgdavdtydtilfakynmpdrkvrifetyligeeaa fadnkkmacankcfprq	420
OY	421	ISTLADVOENWMEYLAVLSRPKVIIOEHVYVMTXAVI DSTFLDDGQVYLMTVPAMVFSK	480
Dp	421	istladvgenwmeylhvlstrpkvldgehdvvtveayidsltlddggvjvmltvpamvfisk	480
OY	481	ONETRSKGIILGVGTDVPVKELEKTIIPKYLGIHQYAFATNNNGYILTHPELRLLYEGB	540
Dp	481	onetrskgillgvvgtdvpvkelektipryklgihqyafatnnngyilthpeltlllyeegb	540
OY	541	KRRKRPNTSVSDLSVEEMEDRDDVLRBNAMVNKRTGTFSEWVKKYDQ:GKRVLYMNTDYYX	600
Dp	541	kkrrkprntsvsdlsveewedrddvrlrnamvnkrtgkfsewvkktyd:gykrvlymtdyyx	600
OY	601	TDIKCTPESLGAVALSRGKGKYPFGRCNVITIEEGILHDL EHPDVSLADENISCNTPDLPENHR	660
Dp	601	tdikctpslgaalstrgkyffrgnvitl eegilndlehpdvsladevsnctndlphehnr	660
OY	661	LSOLEAIFKLYLKGRPELLOQKRELIOEVLFDAVVSAPITAYMTSLAKNSENSCKVEVA	720
Dp	661	lsqleaifklylkgreplloqckelioevlfidavvsapleayvtsla:knssensckgveva	720
OY	721	FLGTRTGSLRILFVGABEOLTMODLLKKGDKCNINFAHDFPLMYRPNAAKOICSFYYSIP	780
Dp	721	flgtrtgslriltfygaeeoltmodllkkaadkenilnadhfplmyrrnaaeqipbsitysisip	780
OY	781	FSTGVNKSNNVTA STSIQILDERSKSPVVAAGIOQMKLEFPORKEWFTASROCASLDGKS	840

Db	781	 f s t p v k s n v t a s t e s i q l l d e k e k a p v y a a v i q n k e f g r k t w s r q s a s d g k s	840
Qy	841	ISCDEYVNC L D N N F I V S E D Y O T G D F E I G A V N K L I N G S F R T T Y D Y A N	900
Db	841	iscde e v n c l d n n f i v s e d y o t g d f e i g a v n k l i n g s f r t t y d y a n	900
Qy	901	CRANKESSDGAHGLDPEYNAFLSAVVKIMTELVLFLVEFNLC S W H S D T A N K O K L O T L	960
Db	901	crankessd g h l d p e y n a f l s a v k i m e l v l f l v e f n l c s w h s d t a n k o k l o t l	960
Qy	961	EPCKTEPAPVPSERTIKET G N I C A C D C S P V I Q I P S N L F N V V D S C E S V A P T	1020
Db	961	epckte p a p v s e r i k e t g n i c a c d c s p v i q i i p s n l f n v v d s c e s v a p t	1020
Qy	1021	MAP E I R N E S L K C E R K A O R R R P E S C H F E N A R E G A S L A O T V L L P L L	1080
Db	1021	map e i r n e s l k c e r k a o r r r p e s c h f e n a r e g a s l a o t v l l p l l	1080
Qy	1081	M E S R	1085
Db	1081	m l f r	1085

RESULT 3
 AAB62248
 ID AAB62248 standard; Protein: 1085 AA.
 AC AAB62248;
 XX
 XX 11-JUN-2001 (first entry)
 DT
 XX Human calcium channel alpha2delta subunit.
 DE
 XX Calcium channel alpha2delta subunit; cerebral cortex;
 KW nervous system disorder; pain; epilepsy; anxiety; human.
 KM
 XX Homo sapiens.
 OS
 PN MO200120336-A2.
 XX
 XX 22-MAR-2001.
 ED
 XX 18-SEP-2000; 2000WO-EP09136.
 PF
 XX 16-SEP-1999; 99US-0397549.
 PR
 XX (WARN) WARNER LAMBERT CO.
 PA
 XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
 PI
 XX WPI: 2001-257902/26.
 DR
 DR N-PSDB; AAF57551.
 XX
 XX Competitive binding assay for screening ligands which bind a cerebral
 PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit,
 PT where the ligands identified are useful for treating disorders of the
 PT nervous system, including pain -
 XX
 XX Disclosure: Page 93-97; 158pp; English.
 PS
 XX The invention relates to a new method for screening ligands which bind a
 CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
 CC preferably alpha2delta-1 subunit. The method comprises contacting a
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of
 CC interest and a labelled compound which binds the subunit, followed by
 CC measuring the level of binding of the labelled compound to alpha2delta-1
 CC subunit. The method is useful for screening ligands, preferably
 CC biologically active products that modulate a nervous system function,
 CC which bind a cerebral cortical voltage-dependent calcium channel
 CC alpha2delta-1 subunit. The ligands identified by the method are useful
 CC for treating disorders of the nervous system, including pain, epilepsy
 CC and anxiety. The present sequence represents a human calcium channel

CC alpha2delta subunit.
 XX
 SQ Sequence 1085 AA:

Query Match 100.0%; Score 5667; DB 22; Length 1085;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1085; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAGPSRRASRGASALLAALLAALGDVVRSEOOPIPLSVKLMASFGCEIKSTAAKY 60
 DB 1 magpsrrasrgasallaaallyaalgdvvrseqqlpsvklwaasaggelkslaaky 60
 OY 61 SGGQLQKKYKEYEKDAIEIDGLQVKKLAKNMEEMFKKSEAVRRLVEAAEALKH 120
 DB 61 sggqlqkkkykeyekdaieelidglqvkklaknmeemfkkseavrrlveaaealakh 120
 OY 121 EPDADLQYEFNAVLINERDKGNFLELCKEFTLAPNDHFNNL.PVNISLSDVOYPTNNYN 180
 DB 121 efdadlqyefnnavlinerdkgnflelckefllapndhfnlpsvlisldvgyptnnyn 180
 OY 181 KDPATVNGYWMSELNKVFVDFNDRDPSLIWOYFGSAKGFROYPGIKWEPDENGVIAPD 240
 DB 181 kdpavngywseelnkvfndfrdpsllwoyfgsakgfroypgikwepdengviapd 240
 OY 241 CRNRKMYIOAATSPKDVILLVDYSGSMKGLRLTIKQTVSSIIDTLGDDDFNNIIAYNEE 300
 DB 241 cnrkmyiaatspkdvillvdysgsmkglrltiakqvssiidtlgdddfnnliaynee 300
 OY 301 LHYVECLNGTLVQADRTNKEHREHLDKLFAKIGMLDIALNEAPNII.SDFNHTGCGST 360
 DB 301 lhyveclngtlvqadrtknehrlhdklfakigmlidalneafnliisdfhtggsst 360
 OY 361 GSAQILITDGAVDYDTJIFAKYNMPDRKVRITFTYLIGREAFADNLKMMACNKGFGFO 420
 DB 361 gsaqilidtgavdydtjifakynmpdrkvrityligrfaadnlkmaacnkgfiftg 420
 OY 421 ISTLADQENVMEXLHVL.SRPKYIDQEHVVMTEAYIDSTLTDDQGPVLTMTTAMPEFSK 480
 DB 421 istladqenvmeylhvl.srpkyidqehvvtteayidstltdqgprvltmttampvfk 480
 OY 481 QNETRSKGLLGVCTVDVYKELKTIPIKXKIGRHGAFATNNGYILTHPELRLLEEG 540
 DB 481 qnetrskgllgvctvdvpykelktipkxkighyafatnngyilthpelrlllyeeg 540
 OY 541 KRRRKPNYSVDLSEVEMEDRDVDLRRNAMYNRKTKFESMEVKTVDKGKVLWMTNDYY 600
 DB 541 krrrkpnysvdlseveMEDRDVDLRRNAMYNRKTKFESMEVKTVdkgkvlwmtndyy 600
 OY 601 TDIKGTPESLGAVALSRGHCKYFFRGNAVTLIEGLHDL.EHPDVSILADEMSYCNTDLHPEHRH 660
 DB 601 tdiKgpEsLgvalsrghkyffrgnavtlieeglhdl.ehpdvsladeWSYCnDlhpehrh 660
 OY 661 LSOLEAIXIKYLKGERPLLOCDKLELOEVLFDVAVSAPIEATWYSLALNSENSENDRKVEVA 720
 DB 661 lsgleaiXikylkgerpllocdkLeolEovLfdvavsapieawtYslalnSensendkveva 720
 OY 721 FLGTRTGLSRINLFVGAEOULTNODFLKAGDKENIFNADHPFLYRRAAEQIPISFYVSTP 780
 DB 721 flgtrtglSrInLFvgaEOuLTnODfLkagDKenIFnaDHPflYrRAAEQIPisfYstP 780
 OY 781 FSTGVPVNSNVVTAJSTSIQLDERKSPVVAAGVIOKMLEFFORKFWTASROCASLDGKGS 840
 DB 781 fstgvpvnsnvvtajstsiQLderKspvvaAGvIOkmlEFForkfwTasrocasldgkgs 840
 OY 841 ISGODETVNCYLIDNNGFLTVSEDTYQTGDFGEIGAVMKNLITMGSKRRTILYIQAM 900
 DB 841 isgodeTVncYLIDnNGflTVseDTyQTgDFgeIGaVMKnLiTMgSKrRTiLYiqAm 900
 OY 901 CRANKESGAGGLDPPYNAFLSAVKWIMTELVLFLVEFNLCGWMHSDPTAKOKOTLT 960
 DB 901 cranKessgagllDppynaflsAvkwImTelvlfLvefnlCGwMhSDptAKoKOTLT 960

OY 961 EPCDTEYPAFVSERTIKETTGNIACEDCSKSFVLIQIPSSNLEPMVVDSSCLCEVAPIT 1020
 DB 961 epcdteypafvserliketTgnIacEdCSksfVliqIPssnLEpmVvdSSclceVapIT 1020
 OY 1021 MAPETIRYNESLKCERKAKIRRRPESCHGFHPEENARCGAPSLQAOVTLLPLLL 1080
 DB 1021 mapetiryneslkcERkAKIRRRPESchGFhPEENARCGAPslQAOvtLLpLL 1080
 OY 1081 MLFSR 1085
 DB 1081 mlfsr 1085
 RESULT 4
 AAU01019
 ID AAU01019 standard; protein; 1065 AA.
 XX
 AC AAU01019;
 XX
 DT 04-JUL-2001 (first entry)
 XX
 DE Human secreted soluble alpha2delta calcium channel subunit #6 protein.
 XX
 KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
 KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
 KW gabapentin; scintillation proximity assay (SPA); nickel flashplate assay;
 KW filter binding assay; wheat germ lectin flashplate assay.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT MISC-difference 1044..1045
 FT /note="Encoded by AGGCCCAAGAATCAGAAGCGC"
 XX
 PN WO200119870-A2.
 XX
 PD 22-MAR-2001.
 XX
 PF 18-SEP-2000; 2000WC-EP09137.
 XX
 PR 16-SEP-1999; 99US-0397550.
 XX
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Brown JP, Bertelli F;
 XX
 DR WPI: 2001-235262/24.
 DR N-PSDB; AAS01409.
 XX
 PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
 PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or
 PT Wheat Germ Lectin Flashplate assays -
 XX
 PS Claim 25; Page 79-82; 160pp; English.
 XX
 CC The present sequence represents human secreted calcium channel
 CC alpha2delta subunit #6 which is soluble and retains the functional
 CC characteristics of the full length or wild type alpha2delta subunit
 CC (AAU01025) from which it is derived. The invention relates to truncated
 CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
 CC which retain their affinity for radioactively labeled gabapentin. The
 CC alpha2delta subunit is 1 of the components of the heteromultimeric
 CC voltage-dependent calcium channel (VDCC) complexes present in neuronal
 CC and non-neuronal tissues including heart and skeletal muscle. Numerous
 CC soluble forms of the human calcium channel alpha2delta subunits
 CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the
 CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are
 CC described. The secreted soluble alpha2delta subunit may be used in assays
 CC e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,
 CC filter binding or wheat germ lectin flashplate assays to detect or
 CC measure the binding or interaction of a ligand (e.g. gabapentin,
 CC L-Norleucine, L-Allo-Isoleucine, L-mechonine, L-Leucine, L-Isoleucine,
 CC L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel

CC alpha2delta subunit.
 XX
 SQ Sequence 1065 AA;

Query Match 98.4%; Score 5577; DB 22; Length 1065;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAGPSRRASGASALLAALLYAALGDVVRSEGOIPLSVKLMASAFGEIKSIKIAKY 60
 DB 1 magpsrrasgasaallaallaalgydvvrseqdipilsvkllwasafgeiklsiaaky 60
 OY 61 SSSQLQKKKYEYKEDVAIEEIDGOLVKLAKNKEEMHKSEAVRIUVEAEAEALKH 120
 DB 61 sssqllqkkkyekedvaeieeidegolvkklaknkeemfhkksaevrllveaeaealhh 120
 OY 121 EFDADLQYEFYNAVLINERDKDNFLLEGEPIIAPNDHFNNLPVNI:LSDVQVPTNMYN 180
 DB 121 efdaqlqyefynaavlinerdkgdnfllgekefilapndhfnlpvnllsdvqptnmy 180
 OY 181 KDPALVNGVYWSLUNKYFVNDPDLINQYFGSAKGFQYQYFGIKPEPDENGVIAD 240
 DB 181 kdpaivngvwslnkyfvndpdlinqyfgsakgffqyqyfgikpepdengviad 240
 OY 241 CNRRKMYIOAATSPKDVVLVDSGSMKGLRLTIKQVTSIIDPTLGDDEFNIITAYNEE 300
 DB 241 cnrrkmyiaaatspkdvvlvdsghmkglrltikqvtsiildptlgsddefniitaynee 300
 OY 301 LHVYPCPLNGTLVQADRTNKEHREHLDKLFAGKIGMDIALNEAFNLLSDFNHTGQGS 360
 DB 301 lhyvpcplngtlvgadrtnkhehrehldklfakgigmldialneafnllsdfnhtgqgs 360
 OY 361 CSQALMLITDGVNRYDITFAKYNNPDRKVRIFTYLIGREAAFPADNLKMACANKCFE 420
 DB 361 csqalmlitdgvdryditaakynnpdrkvriftyligreaafpadnlkmacankcfec 420
 OY 421 ISTLADVOENVNVEYLVHSRPKVIIDOEHDVMTYEAVIDSTLDDGSPVLMYVAMPVFEK 480
 DB 421 istladvoenvnveylhvsrpkviiidoehdvmtyeavidstlddgspvmltvmampvfk 480
 OY 481 QNETRSKILGLGVGTDPVPEKLELTKPIRYKLGIGYAFATINNGYILTHPELRLLYEBG 540
 DB 481 qnetrskilglvgtdvpvkelktkpiyrykligyafatinnngyilthpelrlllyeeg 540
 OY 541 KRRKRPNSVYDLSEVEMEDRDVLRNMAVNRKTGKFSMEVKYTDGKRVLMYMTDYY 600
 DB 541 krrkrpnsydlsevemedrdivlrnmavnrktdgkfsmevktvdkgrvlymtndyy 600
 OY 601 TDIKTPFSLGAVALSRGKGYFFRGNVNTEEGILHDEHFDVSLADPKSYCNLDLHPEHH 660
 DB 601 tdiktpfslgavalsrgkgyffrgnvnteegilhdhfdvsladpksyctndlhpehh 660
 OY 661 LSQLEAIKLYLKGBPLLOCDKELIQEVLFDVNSAPLEAVYMTSLAINSENSDKCEVA 720
 DB 661 lsqleailklylkgbpllocdkelqevlfdvnsapieavymtslainsensdkcevea 720
 OY 721 FLGTGTGSLRIULFVGAEOULTQODPLKADKENIFNADHFPMLRYRAAQIRGSEVYSIP 780
 DB 721 flgtgtgslriulfvgaEOULTQODPLKADKENIFNADHFPMLRYRAAQIRGSEVYSIP 780
 OY 781 FSTGVNNSNVYASTSIQDLDERKSPVYAAVGICMKLEFPQRKFPJASROCASLDGKS 840
 DB 781 fstgvnnsnvastsiqlderkspvyaavgicmklefqrkfpjarsocaslsgks 840
 OY 841 ISCDDETVCYLIDNNGFLTVSEEDYTGTGDFEGELEGAVNNKLLTWGSEKRTILYDQAM 900
 DB 841 iscdetvncylidnnngfltvseedytgtgdfegelegavnnklltwgsekrtilydgam 900
 OY 901 CRANESSDGAAGLLDPINAFISAVKWTETELVLEFVNLCSSWHSMDTAKAOKIKQTL 960
 DB 901 cranessdgaaglldpinafisavkwteetelvllefvnlcswhsmdtakakikqtl 960

OY 961 EPCDTEYPAFVSERTIKETTGNIACEDCSKSFVIOQIPSSNLMFVWSSCLCEVAPIT 1020
 DB 961 epcdteypafvsertikettgniacedsksfvioqipssnlmfvwssclcevapit 1020
 OY 1021 MADIEIRYNESLKCERLKAKIRRPESCHGFPEENARECGAP 1065
 DB 1021 madietiryneslkerlkakirrpeschgfppeenarecgap 1065

RESULT 5
 AAB62243
 ID AAB62243 standard; Protein; 1071 AA.
 XX
 AC AAB62243;
 XX
 DT 11-JUN-2001 (first entry)
 XX
 DE Human calcium channel alpha2delta subunit.
 XX
 KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
 XX nervous system disorder; pain; epilepsy; anxiety; human.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1041..1046
 FT /note="this region is not indicated in the sequence
 provided in the sequence listing"

WO200120336-A2.

22-MAR-2001.

18-SEP-2000; 2000MO-EP09136.

16-SEP-1999; 99US-0397549.

(WARN) WARNER LAMBERT CO.

Bertelli F, Brown JP, Dissanayake V, Suman-Chaunan N, Gee NS;

WPI; 2001-257902/26.

N-PSDB; AAF57546.

Competitive binding assay for screening ligands which bind a cerebral
 cortical voltage-dependent calcium channel alpha2-delta-1 subunit, the
 where the ligands identified are useful for treating disorders of the
 nervous system, including pain -

Disclosure; Page 79-82; 158pp; English.

The invention relates to a new method for screening ligands which bind a
 cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
 preferably alpha2delta-1 subunit. The method comprises contacting a
 secreted soluble recombinant alpha2delta-1 subunit with a ligand of
 interest and a labelled compound which binds the subunit, followed by
 measuring the level of binding of the labelled compound to alpha2delta-1
 subunit. The method is useful for screening ligands, preferably
 biologically active products that modulate a nervous system function,
 which bind a cerebral cortical voltage-dependent calcium channel
 alpha2delta-1 subunit. The ligands identified by the method are useful
 for treating disorders of the nervous system, including pain, epilepsy
 and anxiety. The present sequence represents a human calcium channel
 alpha2delta subunit.

Sequence 1071 AA;

Query Match 98.2%; Score 5564; DB 22; Length 1071;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1065; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

OY 1 MAGPSRRASGASALLAALLYAALGDVVRSEGOIPLSVKLMASAFGEIKSIKIAKY 60

|||||
Db 1 magpsprrasgasallaalaallyaalgdvrsseqjprsvvklwasafgsktsaaky 60
OY 61 SSSQLLQKKYKYEKDVAAIEEIDGLQVKKLAKNMEEMPHKSEAVRRVLEAAEAHLKH 120
Db 61 ssgqlqkkykxeyekdvaleeIdglvkkLaknmeemfhkksaavrrlvaaeeahlkh 120
OY 121 EFDADLOEYEFNAVLINERDKGNFLELGKEFI LAPNDFNNLPVNISLSOVQVFTNMYN 180
Db 121 etfdadlqeyefnavlinerdkgnflelgkefilapndhfnlpvnlsdstvqvtmyn 180
OY 181 KDPALVNGVWSESUNKVYFVNDNEDPSLIWQYFGSANGFERQYRGIKWEPDENGVIAFD 240
Db 181 kdpalvngvwseslnkvfyvndnedpsliwqyfgsangferqyrgikwepdengviafd 240
OY 241 CRNRKWTIOAATSPKDDVTLVDVSSGSMKGLRTIAKQVYSSLTLDLGDDEFNITAYNEE 300
Db 241 crnrkwtioaatspkddvtlvdvssgsmkglrtiakqvysstldldgddfnitaynee 300
OY 301 LHVYPCNLNGTLVQADRTNKEHFRHLDKLFAGIGMLDIALNEAFNILDENHTGOGSI 360
Db 301 lhyvpcnlngtlvgadrtcnkehfrhldklfakgigmldialneafnildstfnhtgogsi 360
OY 361 CSQAIMLTIDGAVDTYTIIPAKYNPDRKVRITFTYLIGREAAFADNLKWMACANKGFETQ 420
Db 361 csqaimitldgavdtytiipakynpdrkvrifttyligreafaadnlkwmacankgffetq 420
OY 421 ISTLADVOENWEYEHVLSRPKVIDEHDVWTFEAYIDSTLTDGDPVLTMTVAMPVSK 480
Db 421 istladvoenweyehvlsrpvldghdvwtfeyayidstltdgdpvltmtvampvsk 480
OY 481 QNETRSKILGLVGTDPVVKELTKTIPKYLIGINGYAFATNNYGLTHNPELRLLYERG 540
Db 481 qnetrskilglvgtdpvvkelktltpkylginyafatnngylthnpelrlllyeeg 540
OY 541 KRRKPNSSVDLSVEWEDRDVLRNANVRKTKGFSMEVAKTYDKGRVLYMTNDIY 600
Db 541 krrkpnssvdlsvewedrdvlnanvrktgkfsmevaktydkgrvlymtndiy 600
OY 601 TDIKTPPSLSGVALSRGKGYFRRGNVTIEGLHDLHPDVSLADWMSQNTDLPEHH 660
Db 601 tdihtpptsigvalsrngkyffrrgnvtieglhlehpdvsladwmsqntdlpehnh 660
OY 661 LSQLEAFLYLGKBPPLQCKDELLQEVLFDAVVASPIEAVYTSALNKSNSDKGVEYA 720
Db 661 lsqleafllylgkepllqcdkellgevlfdavvasapieavvtsalnksnsdkgveya 720
OY 721 FLGRTTGLSRINLEFGAQLTNODFLKAGDKENITNADHFLMYRRAEQIRGSFVYSTP 780
Db 721 flgtrtglsrlnlefgaqltnodflkagdkenitnadhfplyrraeqirgsfvystp 780
OY 781 FSTGVPVNSNVYASTSIQLLDERKSPVAAVGIOMLKEFPORRKMWTASROCASIDGKS 840
Db 781 fstgvpvnsnvystsiqllderkspvvaavgiomlkefporrkmtasrocasiDgks 840
OY 841 ISCODETVNCLIDNNGEFLVSEDTQTQDFEGELEGAVMNKLTMGSFKRTLLDYQAM 900
Db 841 iscodevnclyldnngelflvseddyttqdfegeleavmnkltmgsfkrtllydyqam 900
OY 901 CRANKESSDGAHGLDIPNATLSAVKIMTELVLFLVEPNLCSMMHSDMTAKAQLKQTL 960
Db 901 crankeessdgaHglDipnatlsavkImtelvlflvefnlcswwhshmtakakqlkqtl 960
OY 961 EPCDTEYAPFSEPTIKETTGNIACEDCSKSPVIOQIPSSNLFMVVWVSSCCEVAPPT 1020
Db 961 epcdteyapfseptiketgnIacEdcskspvIoqIPssnlfmvvwsccceavapt 1020
OY 1021 MAPLEIRYNESLKCEERLK-----AOKIRRPESCHGFHPRENAECGAP 1065
Db 1021 mapleiryneslKceerlkagkIrrraqkIrrpeschgfhprenaecggap 1071
RESULT 6

AAU01026
ID AAU01026 standard; Protein: 1077 AA.
XX
AC AAU01026;
XX
DT 04-JUL-2001 (first entry)
XX
DE Mouse wild type alpha2delta-3 calcium channel subunit protein.
XX
KW Mouse: secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VCC;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW filter binding assay; wheat germ lectin flashplate assay.
XX
OS Mus musculus.
XX
PN WO200119870-A2.
XX
PD 22-MAR-2001.
XX
PE 18-SEP-2000; 2000MO-EP09137.
XX
PK 16-SEP-1999; 99US-0397550.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Brown JP, Bertelli F;
XX
DR WPI: 2001-235262/24.
XX
PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays.
PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or
PT Wheat Germ Lectin Flashplate assays -
XX
PS Example 12: Page 101-104; 160pp; English.
XX
CC The present sequence represents mouse wild type calcium channel
CC alpha2delta-3 subunit protein which is used to obtain soluble secreted
CC mouse alpha2delta deletion mutant. The sequence is described in an
CC invention relating to truncated alpha2delta-2, alpha2delta-3 or
CC alpha2delta-4 subunit soluble proteins which retain their affinity for
CC radioactively labelled gabapentin. The alpha2delta subunit is 1 of the
CC components of the heteromultimeric voltage-dependent calcium channel
CC (VCC) complexes present in neuronal and non-neuronal tissues including
CC heart and skeletal muscle. Numerous soluble forms of the human calcium
CC channel alpha2delta subunits (AAU01014-AAU01024 and AAU01032-AAU01038)
CC and 5 soluble forms of the porcine calcium channel alpha2delta subunits
CC (AAU01027-AAU01031) are described. The secreted soluble alpha2delta
CC subunit may be used in assays e.g. scintillation proximity assay (SPA),
CC flashplate, nickel flashplate, filter binding or wheat germ lectin
CC flashplate assays to detect or measure the binding or interaction of a
CC ligand (e.g. gabapentin, L-Norleucine, L-Allo-isoleucine, L-methionine,
CC L-leucine, L-isoleucine, L-Valine, Spermine and/or L-phenylalanine) of
CC a calcium channel alpha2delta subunit.
XX
SQ Sequence 1077 AA;
Query Match 96.3%; Score 5459; DB 22; Length 1077;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1049; Conservative 1; Mismatches 14; Indels 6; Gaps 1;
OY 1 MAGPSPRRASGASALLAALLYAALDGVVSEDOIPLSVYKLTWASAFGCEIKSIARKY 60
Db 1 magpsprrasgasallaallyaalgdvvrseqjprsvvklwasafgsktsaaky 60
OY 61 SSSQLLQKKYKYEKDVAAIEEIDGLQVKKLAKNMEEMPHKSEAVRRVLEAAEAHLKH 120
Db 61 ssgqlqkkykxeyekdvaleeIdglvkkLaknmeemfhkksaavrrlvaaeeahlkh 120
OY 121 EFDADLOEYEFNAVLINERDKGNFLELGKEFI LAPNDFNNLPVNISLSOVQVFTNMYN 180
Db 121 etfdadlqeyefnavlinerdkgnflelgkefilapndhfnlpvnlsdstvqvtmyn 180

QY 181 KDPATVNGVWSESLNKVFVNDPRLIMQYFGSAGKGFPROYPGIKWEPDENGVIAD 240
 DB 181 kdpatingvwyseeslnkvfnvndfdrpslimgyfsagkgyffrtqypgikwepdengviad 240
 QY 241 CRNRKWTIOAATSPKDVVILVDVSGSMKGLRLTIAKQTVSSILDTLGDDDFNIIAYNEE 300
 DB 241 crnrkwyigaatspkdvvilvdvsgsmkgllrtlaqtvssilddtlgdddfnniitynee 300
 QY 301 LHVYEPCLNGTLVQADRTNKEHFRHLDKLFAKGIQMLDIALNEAFNLSDFNHTGQSGI 360
 DB 301 lhyvepclngtlvgadrtnkhefrhldklfakgigmldialneafnlsdfnhgqgsi 360
 QY 361 CSQAIMLTIDGAVDVTDTIFAKYNWPDNRVRIFTYLGREAFAFNLCMAMACANKGFPTQ 420
 DB 361 csqaimgltidgavdvtctifakynwprdkvriftyligreaafadnlkwmacankgfftcq 420
 QY 421 ISTLADVOENWEXLHVLRRPKVIDOEHDVWTEAYIDST-----LIDDOGPVIMTVA 474
 DB 421 istladvgenwexlhlvsrpkvidogehdvwteayidstlpgaqklddggvlmvtva 480
 QY 475 MPVPSKQNETSKGILGAVGTDVPVKELTIPEYKLGIGHYAFATINNGYILTHPELR 534
 DB 481 mpvlskqnetrskgillgvvgtdvpvkeltkipkykigibghafainngyilthpeir 540
 QY 535 LLYEGKRRKPNYSSVDLSEVEMEDRDDVLBNAMVNRKTGKSEMEVKKTVDKGRVLVM 594
 DB 541 pllyegkrrkpnysvsvdlseveemedrddvlnamvnrktgkfsmevkktvdkgrvlyvm 600
 QY 595 TNDYVYTDIKSTPESLGAVALSRGHGKYPFRGNVTIEEGLHDEHNDVSLADEMSKNTDL 654
 DB 601 tndyytytdikstpslgavalsrghgkyffrgnvtieeglhdehndvsladevskntdl 660
 QY 655 HPEHRHLSQLEAIRLYLKGEKREPLQCKEKLQEVLPDAVVASPIAYVITSIALNKSENSD 714
 DB 661 hpehrhlsqleairlylkgekreplqckekleqvlpdavvaspilaayvitsialnksensd 720
 QY 715 KGEVAFIAGTRGSLRILFVGAEOLTNODPLKAGDKENIFADHPPLMYRRAAKOIGSS 774
 DB 721 kgevafagtrgslrilmfvgaeoltnodplkagdkenifadhpplmyrraaeqiags 780
 QY 775 FVYSIPFSTGPNKSNVYASTSIQDLDBRKSPPVAAVGIOKLEFPYRKFWTASROCAS 834
 DB 781 fvyisipfstgpnksnvystsiqlddbbrksppvvaavgioqklefpyrkfwtastrcas 840
 QY 835 LDGKCSICDDETVNCTIIDNNGFTLVSEDTYQTSDFGEGIEGAVMNKLLTNGSKRRTL 894
 DB 841 ldgkcsiscddetvncyliidnngftlvseedytqtgdfgvegavmnrlltngskfrrtl 900
 QY 895 YDYQAMCRANESSDGAHGLDIPYNAFLSAVKWIMTELIVLFVEPNLUSMWSMDTAKAQ 954
 DB 901 ydyqamcranessdgaahglldipykaflsaakwimtelivlfvefnlswmshmdtakag 960
 QY 955 KIKQTLIEPCDIEYPAFVSERTIKETGNIACEDCSKSFVIOQIPSSNLFMVVVDSCLCE 1014
 DB 961 kikqtlepcdieypafvseritketgnilacedcsksfvioqipsnlfmvvdsclce 1020
 QY 1015 SVAPITMAPIEIRYNESLKCEBLKAQKIRRPESCHGFHPEENARECGCA 1064
 DB 1021 svapitmaapieiryneslkerlkaqkrrrpeschgfhppeenarecga 1070

RESULT 7
 AAB62250 ID AAB62250 standard; Protein: 1077 AA.
 AAB62250;
 11-JUN-2001 (first entry)
 Human calcium channel alpha2delta subunit related seq ID No. 24.
 Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;

KN nervous system disorder; pain; epilepsy; anxiety; human.
 XX Homo sapiens.
 OS WO200120336-A2.
 PN 22-MAR-2001.
 PP 18-SEP-2000; 2000WO-EP09136.
 XX 16-SEP-1999; 99US-0397549.
 XX (WARN) WARNER LAMBERT CO.
 PA Bertelli F, Brown JP, Dissanayake V, Suman-Chanuan N, Gee NS;
 DR WPI; 2001-257902/26.
 XX Competitive binding assay for screening ligands which bind a cerebral
 PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit,
 PT where the ligands identified are useful for treating disorders of the
 PT nervous system, including pain -
 PS Disclosure; Page 100-104; 158pp; English.
 XX The invention relates to a new method for screening ligands which bind a
 CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
 CC preferably alpha2delta-1 subunit. The method comprises contacting a
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of
 CC interest and a labelled compound which binds the subunit, followed by
 CC measuring the level of binding of the labelled compound to alpha2delta-1
 CC subunit. The method is useful for screening ligands, preferably
 CC biologically active products that modulate a nervous system function,
 CC which bind a cerebral cortical voltage-dependent calcium channel
 CC alpha2delta-1 subunit. The ligands identified by the method are useful
 CC for treating disorders of the nervous system, including pain, epilepsy
 CC and anxiety. The present sequence represents a human calcium channel
 CC alpha2delta subunit related sequence.
 XX Sequence 1077 AA;
 SQ

Query Match 96.3%; Score 5459; DB 22; Length 1077;
 Best Local Similarity 98.0%; Pred. No. 0;
 Matches 1049; Conservative 1; Mismatches 14; Indels 6; Gaps 1;

QY 1 MAGPSPRASRGASALLAALLYALGDVNSEQDIPLSYVKLWMAFGGEIKSIATARY 60
 DB 1 magpslccasrgasallatallyaalgdvnrseqdiplsyvkklwasafggetksiaaky 60
 QY 61 SSSQLQKKYKEYEKDVAIEETIDGLOLYKKLAKNMEEMHKSEAVRRLVEAAEAGHLKH 120
 DB 61 ssgqlqkkykeyekdvaieeidglolyvkkklaknmeemhkkseavrriveaeaeahlkh 120
 QY 121 EFDADIQEYFNAVALINNEKDGNFLELGEFTLIANDHFNPNLPVVISDVOVPNNMYN 180
 DB 121 efdadiqeyfnavalinnedkgnfllelgeftliandhfnpnlpvisdvpnnmy 180
 QY 181 KDPATVNGVWSESLNKVFVNDPRLIMQYFGSAGKGFPROYPGIKWEPDENGVIAD 240
 DB 181 kdpatingvwyseeslnkvfnvndfdrpslimgyfsagkgyffrtqypgikwepdengviad 240
 QY 241 CRNRKWTIOAATSPKDVVILVDVSGSMKGLRLTIAKQTVSSILDTLGDDDFNIIAYNEE 300
 DB 241 crnrkwyigaatspkdvvilvdvsgsmkgllrtlaqtvssilddtlgdddfnniitynee 300
 QY 301 LHVYEPCLNGTLVQADRTNKEHFRHLDKLFAKGIQMLDIALNEAFNLSDFNHTGQSGI 360
 DB 301 lhyvepclngtlvgadrtnkhefrhldklfakgigmldialneafnlsdfnhgqgsi 360
 QY 361 CSQAIMLTIDGAVDVTDTIFAKYNWPDNRVRIFTYLGREAFAFNLCMAMACANKGFPTQ 420
 DB 361 csqaimgltidgavdvtctifakynwprdkvriftyligreaafadnlkwmacankgfftcq 420

OY	421	ISTLADVENVMEYLAHVLSRPVLDQEHVDVWTEAYIDST-----LTDDCGPVLMTTVA	474
DB	421	ISTLADVENVMEYLAHVLSRPVLDQEHVDVWTEAYIDST-----LTDDCGPVLMTTVA	480
OY	475	MPVFSKONETRSKGLLVGVGTDPVKELLKTIPIRYKLGIGHYAFATINNGSYILTBELR	534
DB	481	mpvfakqnetrskglllgvgvgtdpvkeallktlpiRYKlgighyafatlnngsyilthpelt	540
OY	535	LLYEGGKRRKRNKSSVOLSEYEMDRDVLRLNMAVNNKTKRFSMEYKKTLYDKGRVLVM	594
DB	541	pLYeggkrrkrpnyssvolsewedrdvrltnmavnrtkqkfsmeykvktvdkgkrylv	600
OY	595	TNDYVYTDIKGPFELGVALSRGHCKYFFRCGNVTJEEGLHOLEHPDVSILAEMSGYCNDL	654
DB	601	tnDYvttdtkgpfelgvalsrghkyffrgnvtleeeglhlhlpdvsiladewyctndl	660
OY	655	HEPHRLSQLEAIKLYLKGBEPLDQCEKLIQEVLFDAVVSAPIDEAVYTSIALNKSENSD	714
DB	661	hpehrlsqlealklylkgepldqckelqevlfдавvsapleaytsialnksensd	720
OY	715	KGVEVAFICGTRGSLRNLPFGAEULTNQDLKAGDKENITNADHFLMYTRRAAEQIPGS	774
DB	721	kGvevaficgtrgslsrnlpfgaegultnqdlkagdkenitnadhflmytrraaeqlags	780
OY	775	FVYSIPEFGTPPNKSNVNTASTSIDLDERKSPVYAAVGIDMKLEFQORKPMTASROCCAS	834
DB	781	fVysipEfgtgvtnksnvntastsiqlldertspryaavgidmkleffqrkhwtsrqcas	840
OY	835	LDGKCSICDDETVNYCYLIDNNGFLLVSEDTYQTGDFEGELIEGAVMNKLLTMSGFKRITL	894
DB	841	ldgksisicddetvncyilidnngfllvseedytqctgdfegevagvmnklltmgsfkrifll	900
OY	895	VDYQAMCANKNESSGAGGLLDPRVAFSLAAYKIMTELYELFVFNLCSMWHSMTAKAQ	954
DB	901	ydyqamcanknessagsangllDpykaflsaakwlmteylivelfvfnlcswwhsdmtakq	960
OY	955	KLKQGLPEPCDTEYPAFVSERTIKETTCGNIACEDCSKFVIOQIPSSNLFMVVDSQCICE	1014
DB	961	kLkqglpecdteypafvserctiketctgnIacedsksfvIqbpasnlfmvvdsqcice	1020
OY	1015	SVAPITMAPIEIRVNESLKCERLKAQKTRRRPESCHGFHPENARECGGA	1064
DB	1021	svapitmapieirvneslkcerlkqktrrrpeschgfhpeanarecggga	1070
RESULT 8			
AAU01018			
XX	ID	AAU01018 standard; Protein; 1038 AA.	
XX	AC		
XX	AAU01018;		
XX	DT	04-JUL-2001 (first entry)	
DE	XX	Human secreted soluble alpha2delta calcium channel subunit #5 protein.	
XX	XX		
KW	XX	Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;	
KW	XX	alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;	
KW	XX	gabapentin; schinlilation proximity assay; SPA; nickel flashplate assay;	
KW	XX	filter binding assay; wheat germ lectin flashplate assay.	
XX	XX		
XX	OS	Homo sapiens.	
XX	PN	MO200119870-A2.	
PD	XX	22-MAR-2001.	
XX	XX		
XX	PF	18-SEP-2000; 2000WO-EP09137.	
XX	PR	16-SEP-1999; 99US-0397550.	
XX	XX		
XX	XX	(WARN) WARNER LAMBERT CO.	

PI Brown JP, Bettelli F;
XX
DR MPI: 2001-235262/24.
N-PSDB: MAS01408.
XX
XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays.
PT Flashplate assays, Nickel flashplate assays, Filter binding assays or
XX Wheat germ lectin flashplate assays -
PS
XX
XX Claim 25; Page 75-79; 160pp; English.
CC
CC The present sequence represents human secreted calcium channel
CC alpha2delta subunit #5 which is soluble and retains the functional
CC characteristics of the full length or wild type alpha2delta subunit
CC (AA001025) from which it is derived. The invention relates to truncated
CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
CC which retain their affinity for radioactively labeled gabapentin. The
CC alpha2delta subunit is 1 of the components of the heteromultimeric
CC voltage-dependent calcium channel (VCC) complexes present in neuronal
CC and non-neuronal tissues including heart and skeletal muscle. Numerous
CC soluble forms of the human calcium channel alpha2delta subunits
CC (AA001014-AA001024 and AA001032-AA001038) and 5 soluble forms of the
CC porcine calcium channel alpha2delta subunits (AA001027-AA001031) are
CC described. The secreted soluble alpha2delta subunit may be used in assays
CC e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,
CC filter binding or wheat germ lectin flashplate assays to detect or
CC measure the binding or interaction of a ligand (e.g. gabapentin,
CC L-Norleucine, L-Allo-Isoleucine, L-methionine, L-leucine, L-Isoleucine,
CC L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel
CC alpha2delta subunit.
XX
XX Sequence 1038 AA;

Query Match	Similarity	95.7%	Score 5422	DB 22	Length 1038
Best Local	Similarity	100.0%	Pred. NO. 0		
Matches 1038	Conservative	0	Mismatches	0	Indels
					Gaps
					0
QY	1	MAGPSPRRASGAGALLAALLAALLAALGADVNSEEOQIPLSVYKTLWASAFGCEIKSTAAKY	60		
Db	1	magpsprrasgsaallaaellaaellaaellgadvnrseqgiprsvkikwasafgsklsaaaky	60		
QY	61	SGSOLLQKKYKEYEKDVAIEEIDGQLVKKLLAKNMEMFHKKSEA VRRLVEAAEBAHLKH	120		
Db	61	sgsgllqkkkykeyekdvaaeeidgqlvklaknmeehfkkseavrrlveaaeeahlkx	120		
QY	121	EEDDALQVEYFAAVILINEDKDNFLEIGKEPILPNPHFNPLPVNISLSDVQVPTNNYN	180		
Db	121	eiddalqveyfaavilinedkdglnlelgeketilapndhfnlpynlslsdvqplmyn	180		
QY	181	KDPAIVNGVYGESESLNKVFDFNDRDPSLIIMQYFESAKGFRRQYGCIMWEPDENCVIAFD	240		
Db	181	kdpaiavgvygeeslnkvfdnfrdpsliimqyfesakgffrrqygcimwepdengvialfd	240		
QY	241	CNRKRWYIOAATSPKDVVILNDVSGSMKGLRLTIKQTVSSILDLPLGDDDFPNITAYNEE	300		
Db	241	cnrkrwyioaatspkdvvilndvsgsmkglrltikqtvssildpllgdddfpnitaynee	300		
QY	301	LHYEPCINGTLVQADRNKKEHREHLKLFKKGIMDIALNEAFNLTSDPNHNGGOSI	360		
Db	301	lhypcnglgtlvqadrfnkenhrehlklfakgigm dialneafnltsdphnggpsi	360		
QY	361	CSOAILMLITDGAVDVDTYIFAKYNMPDRKRVRITFYTLIGREAFAFADNLKMMACANKGPTQ	420		
Db	361	csqailmlitdgvdcydtlftakynmpdrkvriflyligr eaafadnlkmmcaankgftq	420		
QY	421	ISTLADVOENWKEYLHVLSPKRVIDQEHVDVWTEAY IDSTLTDDGPLYLMTTVAMPVFSK	480		
Db	421	istladvgenwkeylhvlspkrvidqehdvwteayidstltdddgpylmttvampvfesk	480		
QY	481	QNEFSSKGIILGAVGTDPVVKELLTKIRYKLGINGVAFATNNQYILTHEBRLLYEEG	540		
Db	481	qnefsskgiilgvavtgvvkeelltkirkykgingvafatnnyilthbedrllyeeg	540		

Oy	541	KKRRKPNSSVDLSEVMEEDRDYLRRAAMNRRKTRGFSMEVKKTVKGRVLYMTNDYY	600
Db	541	kkrrkpnysvdlsewewedtrddvllramwnrktgkfsmevkktvdkgrtvlvmtndyy	600
Oy	601	TDIKGTFFPSLGVALSRSRGKFFKFFGNVTIEEG,LHDE,HPVSLADMKSCNTDLPHEHH	660
Db	601	tdiigtptfsigvalrsybhgyffirgnvtieeg,lhdl ehpvsladewyscndllpnehh	660
Oy	661	LSQLEAIKLYLKGEPLLCQDKELIQEVLDAVVASPIEAWTSLALNSENSDKGEVA	720
Db	661	lsqleaitklykgeplllqcdkeliqevlfdavvasapieawtslalnksensdkgeva	720
Oy	721	FLGRTRTGSRLNFVGAEDLTNDQFLKAGCKEINFNADRPMLYRRALQIPGSFYSTP	780
Db	721	flgrtgrtsrlnlfvgaedltndqflkagckeni fnadrlplyrraaeqipgsfysfip	780
Oy	781	FSTGPVKNSSNVVASTSTIOLDERKSPVVAAGIQMKLEPFQKFWTASNOCASLDGKCS	840
Db	781	fstgpvknssnvstastsiglllderkspvvaagvayiqmkleffqkftwstsgcasldgkcs	840
Oy	841	ISCDDETVCNLYLDNNNGFVLIVSEDTQGTQGFGEIGAGVANKLLLTGSKFRKITLXDYQAM	900
Db	841	iscddetvncylldnnngfvlivsedytqgtqgfgeigavmankllltngskfrkitllydynam	900
Oy	901	CRANKESDDGAHGLDPRYNAFLSVKRMIMELVLFVERFLCSWMHSIDMTAKAOKLQTL	960
Db	901	crankessdgaahglldpynaflsavkwimtelvlfvefnlcswmshmtakagkllqtl	960
Oy	961	EPCTEYPAFSERTIKETTGNICEDCSKSPFIOOIPSSNLEPMVWVSDSCCESVAPIT	1020
Db	961	epcteypafseretikettgtniacedcsksfviqgipssnlmvmvvasccesvapit	1020
Oy	1021	MAPIEIRYNESLKGERLK 1038	
Db	1021	mapieiryneslkcerik 1038	
RESULT	9		
AAB62242	ID	AAB62242 standard; Protein; 1038 AA.	
XX	AC	AAB62242:	
XX	XX		
DT	11-JUN-2001	(first entry)	
DE	Human calcium channel alpha2delta subunit.		
XX	Ca ²⁺ channel alpha2delta subunit; alpha2delta-1; cerebral cortex;		
KW	nervous system disorder; pain; epilepsy; anxiety; human.		
XX	Homo sapiens.		
OS			
PN	MO200120336-A2.		
XX			
PD	22-MAR-2001.		
XX			
XX	18-SEP-2000; 2000WO-EP09136.		
PF			
XX	16-SEP-1999; 99US-0397549.		
PR			
XX			
PA	(WARN) WARNER LAMBERT CO.		
XX			
PI	Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;		
XX	WPI; 2001-257902/26.		
DR	N-PSDB; AAF57545.		
XX			
PT	Competitive binding assay for screening ligands which bind a cerebral		
PT	cortical voltage-dependent calcium channel alpha2-delta-1 subunit,		
XX	where the ligands identified are useful for treating disorders of the		
XX	nervous system, including pain -		

PS	Dislosure:	Page 76-79; 158pp; English.
XX	The invention relates to a new method for screening ligands which bind a	
CC	cerebral cortical voltage-dependent calcium channel alpha2delta subunit,	
CC	preferably alpha2delta-1 subunit. The method comprises contacting a	
CC	secreted soluble recombinant alpha2delta-1 subunit with a ligand of	
CC	interest and a labelled compound which binds the subunit, followed by	
CC	measuring the level of binding of the labelled compound to alpha2delta-1	
CC	subunit. The method is useful for screening ligands, preferably	
CC	biologically active products that modulate a nervous system function,	
CC	which bind a cerebral cortical voltage-dependent calcium channel	
CC	alpha2delta-1 subunit. The ligands identified by the method are useful	
CC	for treating disorders of the nervous system, including pain, epilepsy	
CC	and anxiety. The present sequence represents a human calcium channel	
CC	alpha2delta subunit.	
XX		
SQ	Sequence 1038 AA;	
	Query Match 95.7%; Score 5422; DB 22; Length 1038;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MAGPGSPRRASGASALALAAALVYALGDPVYSEDOIPLSVYKLMASAFGEIKSIAAKY 60	
DB	1 magpgsprasrsgaasallaalaaalgaagvrseqdiprsvyklwasatfgyslkslaaky 60	
QY	61 SSGQLQKKYKEYEKDVAIEETIDQLVYKLAKNMEEMHKSEAVRRLVEAEAHLLKH 120	
DB	61 ssgsqlikkkykeyekdvaieetidqlvkkaklmmeeemhkkseavrrlveaeaaahllkh 120	
QY	121 EPDADLQYEFYFAVALINEDKGNFELCEKETLAPNDHFNNLPNVISLSDVQVPTNMVN 180	
DB	121 efdadlqyefyfaivalinedkgnfelceketlilpnndhfnnlpnvislsdvqvpntmyn 180	
QY	181 KDPALVNGVYSESLNKVFDFNDRDPSLIWIQYFGSAGKFPFQYQGIKWEPDENGVIADF 240	
DB	181 kdpalvngvyseeslnkvdfndrdpsliwiyfgsakgfpfpyqgiikwepdengviadf 240	
QY	241 CNRRKKYIOAATSPKRVVILVYSGSMKGLRTIAKQYTSILDTFGDDPFNTIAYNEE 300	
DB	241 cnrrkkyidaatspkcvvillvsgsmkglrtiliaqvtslldtfgddfnlilaynee 300	
QY	301 LHYVEPCNLGTVOADRTNKEHREHLDLFAKIGIMDLIALNEAFNIIIDENHTGQGI 360	
DB	301 lhyvepcnlgtvadrtnkehrehldlfaigyimdlialneafniiidfnhtggsi 360	
QY	361 GSOALMLITDGAVDYDITFAKYNMPDRKVRIFPTYLIGBAAPADNLKMAKANGPFQ 420	
DB	361 gsoalmilitdgavdydtilfakynmpdrkvrifptyligbaafadnlkmaakangfifq 420	
QY	421 ISTLIAVOENWMEYLHVLRSRPVYIDDEHHVWVTEAVIDSTLFDGQPVLMTVAHVESK 480	
DB	421 istliavoenwmeylhvlrsrpvqiddehhvvtteayidstliddgqpvmltvaavfesk 480	
QY	481 QNETRSKGLLGAVGTDVPEKELKTIPYKLGIGHYAFATNNNGYILTHPELRLLYEEG 540	
DB	481 qnetrskglllgavgtadvpekelktlipykllgihyafatnnngyilthpelrlllyeeg 540	
QY	541 KRRRRKNYSVDSLSEKEMDRDDVLRNANVNRKTKGFSMEVKKTYDKGRVLYWINDYY 600	
DB	541 krrrrknysvdsleskemdrrddvlnanvnkrkkgfismevkktydkgrvlywimndyy 600	
QY	601 TIKGTGFSFLGVALSKGSKYFGRGNTLTIEGLHDLNHDVSLADWSYCNTDLPHNRH 660	
DB	601 tidktgfsflgvalskgskyffgrgntltieglhldnhdvsladwsycntdlphnrh 660	
QY	661 LSQLEAKIKLYLKGKEPLLOCDKELLDEVLPDAVNASPFIATYTSIALNKSEMSDKGVFA 720	
DB	661 lseqleakiklylkgkepllqcdkellqevlfdavnaspileaytsialnksensdkgvfa 720	
QY	721 FGTGTRGSLRINLFGAEOQLTNODFLAKADKNIFINADHFFPLMYRRAAEOIGSFVYSIP 780	

Db 841 iscdetvncylidnngfllysedytqtdffgelegavmklcmg:fkritllydyqam 900
QY 901 CRANKESSDGAHGLDPYNAFLSAVKWIMTELVLFLVEPNLCSMWSHMTAKAQIKQTL 960
Db 901 cranekessdgaahglldpynaflsavkwimtelvlflvefnlcswwshmtakqkql 960
QY 961 EPCDTEYPAFVSERTIKETGTGNACEDCSKSFVIOQIPSSNLFMYVVDSSCLCESVAPI 1019
Db 961 epcdteypafvserliketgtgnacedcsksfviqipsnlfmyvvdssclcesvapi 1019
RESULT 11
AAB62241
ID AAB62241 standard; Protein: 1019 AA.
AC AAB62241;
XX 11-JUN-2001 (first entry)
DE Human calcium channel alpha2delta subunit.
XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
KW nervous system disorder; pain; epilepsy; anxiety; human.
XX Homo sapient.
OS
XX MO200120336-A2.
PM 22-MAR-2001.
PD 18-SEP-2000; 2000MO-EP09136.
XX 16-SEP-1999; 99US-0397549.
PR (WARN) WARNER LAMBERT CO.
XX Bertelli F, Brown JP, Dissanayake V, Suman-Chanhan N, Gee NS;
PI WPI: 2001-257902/26.
DR N-PSDB; AAF57544.
XX Competitive binding assay for screening ligands which bind a cerebral
PT cortical voltage-dependent calcium channel alpha2delta-1 subunit,
PT where the ligands identified are useful for treating disorders of the
PT nervous system, including pain -
XX
XX Disclosure: Page 72-75; 158pp; English.
PS The invention relates to a new method for screening ligands which bind a
CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
CC preferably alpha2delta-1 subunit. The method comprises contacting a
CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of
CC interest and a labelled compound which binds the subunit, followed by
CC measuring the level of binding of the labelled compound to alpha2delta-1
CC subunit. The method is useful for screening ligands, preferably
CC biologically active products that modulate a nervous system function,
CC which bind a cerebral cortical voltage-dependent calcium channel
CC alpha2delta-1 subunit. The ligands identified by the method are useful
CC for treating disorders of the nervous system, including pain, epilepsy
CC and anxiety. The present sequence represents a human calcium channel
CC alpha2delta subunit.
XX
XX Sequence 1019 AA;

Query Match 93.9%; Score 5324; DB 22; Length 1019;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGPSPRRASGASALAAALLVYALGDVRSSEQOIPLSVYKWLWASAFGEIKSIANY 60
Db 1 magpsprrasgasalaaallvyaalgdvrsseqiplsvkwlasafgeiksiaky 60

QY 61 SCSQLQKKRYKEYEKXDVAIEETDGLQLVKKIAKNMEEMFKKSEAVRRLVEAEAEALKH 120
Db 61 ssgqlqkkykeyekxdvaeieetdgllvkklaknmeemfkkseavrrlveaeaealkh 120
QY 121 EFDADLOVEYFNAVLINERDKDGNFLELKEFLLAPNDHFNNLPVNIISDVQVPTNMYN 180
Db 121 efdaadloyeyfnavlinderkdgndfellekefllapndhfnnlpvnlisdvqvpntnmy 180
QY 181 KDPALVNGVYWSSESLKVVVDNFDPRPSLIWQYFGSAKGFERYPCIKMEPDENGYIAD 240
Db 181 kdpalvngvywseslnkvvdnfdprpsliwqyfgsakgferypcikmepdengyiad 240
QY 241 CRRRKWYIOAATSPKDVVLIVDVGSGMKGLRLIAKQVSSILDITDGDDEFNIILAYNEE 300
Db 241 crrrkwyioaatspkdvvlivdvsgsmkgllrliaqvssilditdgddefniilaynee 300
QY 301 LHYVEPCLNGTLVQADRTKNEHREHDLFAKIGIMDLIALNEAFNIIISDFNHTGOGSI 360
Db 301 lhyvepclngtlvqadrtnkehrehldkfakgigmldialneafniiisdfnhtggsi 360
QY 361 CSQAIMLTIDGAVDYDTIPAKYNMPPDKRYRFTYILIGREAPADNLKMACANKGFPTQ 420
Db 361 csqaimgltidgavdydtifakynmpdkryrftyligrapadnlkmacankgfftq 420
QY 421 ISFLADVQENVMEXLHVLSRPKYIDQEHVYVWEAYIDSTRLTDGQPVLMTTVAMPVFSK 480
Db 421 isfladvqenvmeylhvlsrpkyidqehvdyvweayidsrltdgqpvmlttvampvfsk 480
QY 481 QNETRSKGLILGVGTVDPVKKELKTIPYKLGIGHYAFATNNGYILTHPELRLLYEES 540
Db 481 qnetrskglllgvgtdvpkkelktipyklgighyafatnngyllthpelrlllyees 540
QY 541 KRRKRPNYSSVDISEVEMEDRDDVLRNAMYNRKTKGFSEMKVTKVVKGRVLYMTDYY 600
Db 541 krrkrpnyssvdisevemedrddvlnamvnrktkgfsmekvtkvkgrvlymtddy 600
QY 601 TDIKGPFSIGVALSRGHGKYPFRGNVTEEGJHDLHPVSLADMSKCNTPDLHPHNRH 660
Db 601 tdi kgpfsigvalsrghgkyfrgnvtleegjhdhpvsladmskcntpdlhpnh 660
QY 661 LSQLEAIKLYLKGEPLLOCDELIOEVLFDVAVSAPIEAYMTSLALNKSSENSDKGEVA 720
Db 661 lsqleai klylkg epllocdelioevlfdvavsapieaymtslalnksensdkgeva 720
QY 721 FLGTRGLSRINLFGAEQTLTNDFLKAGDKENIFNADHPPLMYRRAAEQIPCSFYVSLP 780
Db 721 flgtrgl srinlfgaeqltndfllkagdenifnadhpplmyrraaeqipcsfyvslp 780
QY 781 FSTRGPVKNKSNVYATRSIQULDRKSPVVAAVGTOIKLEFFORKFMTASROCASLDGKS 840
Db 781 fstrgpvknksnvyaatsiquldrkspvvaavgtoiklefforkfmtasrocasldgks 840
QY 841 ISCDDETVCNLCYLLIDNNGFLIYSEDYOTGDFEIEIGAANVANKLLTGTGSEFKRILYDQAM 900
Db 841 iscdetvncylidnngfllysedytqtdffgelegavmklcmg:fkritllydyqam 900
QY 901 CRANKESSDGAHGLDPYNAFLSAVKWIMTELVLFLVEPNLCSMWSHMTAKAQIKQTL 960
Db 901 cranekessdgaahglldpynaflsavkwimtelvlflvefnlcswwshmtakqkql 960
QY 961 EPCDTEYPAFVSERTIKETGTGNACEDCSKSFVIOQIPSSNLFMYVVDSSCLCESVAPI 1019
Db 961 epcdteypafvserliketgtgnacedcsksfviqipsnlfmyvvdssclcesvapi 1019

RESULT 12
AA92321
ID AA92321 standard; Protein: 1120 AA.
AC AA92321;
XX 10-AUG-2000 (first entry)
XX

DE Human alpha-2-delta-D calcium channel subunit.
XX alpha-2-delta-D; calcium channel subunit; 3p21.1; gabapentin; cytostatic;
KW anticonvulsant; antimigraine; antiparkinsonian; antidepressant.
XX
OS Homo sapiens.
XX
PN M020020450-A2.
XX
PD 13-APR-2000.
XX
PE 07-OCT-1999; 99MO-US23519.
XX
PR 07-OCT-1998; 98US-0103322.
PR 30-OCT-1998; 98US-0106473.
PR 29-DEC-1998; 98US-0114088.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI John MA, Molder B, Offord JD;
XX
DR WPI: 2000-303744/26.
DR N-PSDB; AAA09254.
XX
PT New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
PT proteins, useful in the treatment of epilepsy, migraine, chronic pain,
PT anxiety, multiple sclerosis or cancer
XX
PS Claim 8; Page 67; 88pp; English.
XX
CC The alpha-2-delta-D gene encodes a calcium channel subunit polypeptide.
CC The gene has been mapped to chromosome 12p13.1. This gene and the related
CC alpha-2-delta-C and -B genes are useful for protecting mammalian cells
CC from abnormal calcium flux by introducing expression vectors containing
CC the respective gene into mammalian cells. The antisense genes are also
CC useful for treating or preventing epilepsy. The alpha-delta-2-A protein
CC is a high-affinity binding target of the anti-convulsant drug gabapentin.
CC Therefore, alpha-delta-2 proteins may also be targeted to treat
CC seizure-related syndromes, migraine, ataxia, vestibular defects, chronic
CC pain, sleep interference, anxiety, amyotrophic lateral sclerosis (ALS),
CC multiple sclerosis, mania, tremor, parkinsonism, substance abuse or
CC addiction syndromes, mood, depression or cancer.
XX
SQ Sequence 1120 AA:

Query Match 62.0%; Score 3515; DB 21; Length 1120;
Best Local Similarity 59.8%; Pred. No. 1.8e-289;
Matches 644; Conservative 194; Mismatches 225; Indels 14; Gaps 6;

QY 15 SALLAALVLAALDGVVRSEQOILPSVVKLWASAFGEIKSIAMKYSGLLQKKYKEE 74
DB 34 SALLWILLIGSLIP-awgqakrlpletvklwdfgdllyltvckysglllqkkykay 92
QY 75 KDVAIEETDGLTKKLLAKMEEMFKKSEAVRRLVEAAEENLKHEDDALQYETENAV 134
DB 93 SSKIEEVDGLYVKTSedemmlrtkveavqnlveaaeadlnheteslvtdygnsv 152
QY 135 LINERDKGNLELGEKEITLAPNDHFNNLPVNISLSDVQVPTNNMKRPALVNGVYSES 194
DB 153 llnerdekgntvelgaelllesnahfnlpyntslssvqlprtnynkprddllngvymsea 212
QY 195 LNKFEVDNFDPSLIMQVFGSAGKFERQYPCIKWEPDENCVIAFDCNRKRWYIOATSP 254
DB 213 lnavfvenfgdpcrltwqfysatcgffclpygikwtpdengvltfdccrnrgvygaatsp 272
QY 255 KDQVILVDVSGSMKGLRTIKAKOTVSSILDTLGDGDPFNITAYNEELHYVPCLANGTIVQ 314
DB 273 kdqvlvldvsgsmkglrtikakotvssiltldtldgddfnitayneelhyvpcclngtivyq 332
QY 315 ADNRNKEFRHRLDLFAKSGIGMLDIALNEAFNLSDPNHTGSGISGQALMLITDGAVD 374
DB 333 adnrnrehfklilveelnvkvgyvvdqalreaflklkqfgeakgsicnqalmlisdgave 392

QY 375 TYDITFANYNMPDRKVRIFTYLLIGREAAFDNLKWMACANKGEFTQISTLADQVENMEY 434
DB 393 dyepfeyknwpcdkvrvfylligresfadrmkwlacnkyqisltdtqgnvmev 452
QY 435 LHVLSRPKVIDEHDVWVTEATIDSTLDDGCP--VLMTVAMVPFSQONERSGILLG 492
DB 453 lhwlsrpkvldedhdvwtvteatidstlddgcp---vlmtvamvpfsqonersgillg 512
QY 493 VVGTDVPVKELKTTPKKRLGIGHYAFATNNGYLLITPELRLVLEEGRK-RRKNYSV 551
DB 513 vvgsdvalrelmklepriklyghyafintnngyllshpdlrplyregkllkpkpnyvsv 572
QY 552 DLSEVEDRDVDLBNAMVNRRTGKFSMEKRTVDGKRRLVMTNDYTYTIDIKGTPFSLG 611
DB 573 dlsevedrdgaelrtamlnreltclsmdvkvmckkyrlyfltdnyfftdlstdtpefslg 632
QY 612 VALSRGKGYFFRGVNTTIEGLHDEHPDVSADMSVSCNDLHNEHRLSLEAKLYL 671
DB 633 vlslrgkgyffrgvnttiegldhdehpdvsladmsvscndlhnehrlsleaklyl 692
QY 672 KGKEPLLOCDELIOEVEFDVAVSAPFAVMTSLALNKSENSDCVEVAFLGTPGLSRI 731
DB 693 tkqdpdlcedelvreylvldavvtapmeayvtalnmseeenhvdmaligtqglirs 752
QY 732 NLFVGAEOILTNDQFLKAGDKENIFNADHFPWYRRABQIPGSFYYSIPFTGP--VYKS 789
DB 753 nlfvgskevdstkltpdeaeavfcldrfplyrqasehpagsfvfnlrwaegpesagep 812
QY 790 NVYTAISTISQILDERKSVYVAAGVGMKLEFFQKRFWRASRQASLDKCSICDDEVN 849
DB 813 mvyltaslvavtvdrrtlaaagvymklefqrkfwatrcstlvdpctscdsld 872
QY 850 CYLDNNGEFIVSEDTYGTGDFGEIEGAVMNKLLTMGSFKRITLYDYQAMCRANKESSD 909
DB 873 cylvdnngefivsedtygtgdfgeiegavmnlklltmgsfkritydyqamcrankesshs 932
QY 910 GAHGLDIPYNAFLSAVKIMTELVLVEFNLC-SWMSHSDMTAKA-----QKLKQLE 961
DB 933 aagpvlpslfafltatryllgelyvllflewswgswydrgeaksvfnshkhhkqdbly 992
QY 962 PCDFEYPAFVSEBRTIKETTGNIACEDCSKSPYIOIPSSNLFMYVDDSCCESVAPITM 1021
DB 993 pcdfeypafvsebrtikettniacedcsksfyoipssnlfmyvddscsesvapitm 1052
QY 1022 APIEIRYNESLKCERLKAQKIRRPESCHGPHPENARECGGAPSLAQOTVLLPL 1078
DB 1053 ateekynasvkcdrmsqklrrrpsdschafpenaqdcgsadstsspplllllpv 1109

RESULT 13
AAU01038
ID AAU01038 standard; Protein: 1097 AA.
XX
AC AAU01038;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human secreted soluble alpha2delta calcium channel subunit #18 protein.
XX
KW Human: secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW filter binding assay; wheat germ lectin flashplate assay.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 747..749
FT FT /note="Encoded by GCTGCG"
FT FT Misc-difference 763..764
FT FT /note="Encoded by TCCGAGTGGCTCCGAGAGGTCTCCGAC"
FT FT CTTCGTGCTGGCTCCGAGAGGTCTCCGAC"

xx Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
xx WPI; 2001-257902/26.
DR
xx
xx
xx Competitive binding assay for screening ligands which bind a cerebral
PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit,
PT where the ligands identified are useful for treating disorders of the
PT nervous system, including pain -
xx
xx
xx Disclosure: Page 154-157; 158pp; English.

xx The invention relates to a new method for screening ligands which bind a
CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
CC preferably alpha2delta-1 subunit. The method comprises contacting a
CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of
CC interest and a labelled compound which binds the subunit, followed by
CC measuring the level of binding of the labelled compound to alpha2delta-1
CC subunit. The method is useful for screening ligands, preferably
CC biologically active products that modulate a nervous system function,
CC which bind a cerebral cortical voltage-dependent calcium channel
CC alpha2delta-1 subunit. The ligands identified by the method are useful
CC for treating disorders of the nervous system, including pain, epilepsy
CC and anxiety. The present sequence represents a human calcium channel
CC alpha2delta subunit.
xx
xx

S0 Sequence 1097 AA;

Query Match 61.5%; Score 3482.5; DB 22; Length 1097;

Best Local Similarity 60.0%; Fred. No. 1e-286;
Matches 638; Conservative 194; Mismatches 217; Indels 15; Gaps 7;

QY 15 SALLAALLLYAALGDVNSEQOIPLSVYVYKMAAFSGEIKSIKAYSGSOLQKKKEYE 74
DB 34 sallwlllllgtslsp-awgqekipletvklwadtfgdlyncvtvysglllqkkykdvge 92
QY 75 KDVAIEETIDGLOLVKLLAKMEEMFHKSSEAVRLVEAAEAAHLKEFDADLOEYFNAY 134
DB 93 salkleevdgletvirkfseadmenlrtrveavqnlveaaeeadlnhefneslvfdynav 152
QY 135 LINEBDKGNFLELGEKFEPLAPNDHFNPLPVNISLSDQVPRNMNKDQATNGYVMS 194
DB 153 llnedegntveelgaeflllesnahnfshpvtsslsvqlrcnyvnykdpdlngvymsa 212
QY 195 LNKYFVDFNDRDPSLIWQYFGSAGFFROYPGIKWEPDENGVIADCRKRYIAAATSP 254
DB 213 lnavfvenfgdprlltwqfygsatgffilypgikwtrpdengvlttdcnnrgyiaqatsp 272
QY 255 KDVTLLVNVSGSMKGLRLTIKQTVSSILDTLGDDEFNIIAYNEELHAYVEPCLNGTLVQ 314
DB 273 kdvlvllvngsgsmkglrltiakotvssiltdtldtigndfvniilayndvnylepckfxllvq 332
QY 315 ADRTKKEHREHLDLKFAKIGIMDLIALNEAFNLSDFNHTGSGISQAIMLITDGAAND 374
DB 333 adrtkrehfkliveelmkvgvvdqalreaqlkqfqaqgslnqgalmsldgave 392
QY 375 TYDTIFAKYNPDRKVRITFTYLGREAFAADNLKMACANKGFQOISTLADVOENVEY 434
DB 393 dyepfeykynpdcvkrryftyligrevsfadrmkacnhygytqslstldatqenmey 452
QY 435 LHVLSRPKVIDQEHVDVTEAVYIDTLTDGCP--VLMTVAMPVFSKONETRSKGLLG 492
DB 453 lhvlsrpnvlhndhlivceaymsklllsqagslcliltvampfskknetsrhglllg 512
QY 493 VVGTDVPVKELTKTPKKGKLGHCYAFATNNGYILTHRELRLLYEEBKK--RRKNYSYV 551
DB 513 vvgtdvavlrclmklapryklyghyaflnctngyllshpdlrplyregkklkpkpnyhsv 572
QY 552 DLSEVEMEDRDVLRNAAVNRKTKFSMEVKTKVGRVLVMTDYTYTDIKGTFPSIG 611
DB 573 dlsevewedqeslrtnmtnetqclsmdvkymdkykrvflfntdyftldstlspstlg 632

QY 612 VALSRGCHGYFFRGVNTVIEGLHLEHPDVSLADEMSYCNCTDLHPEHRLSOLEAIKLYL 671
DB 633 vlvsrghgylllgntsvveegldhllpdlatalagdwlycldtdpdkrlslsqleamtrfl 692
QY 672 KGKEPLOCDDKELIOEVLEDAVVSAPIEAVWTSLANKSENSDKGEVAFGLGR--TGLSR 730
DB 693 tkdkploedeevtrvllldavvtapmeayvtalalmseeehvvdmaflgtrsglllr 752
QY 731 INLFVGAELTQNDQFLKADGKKEIFNADHFPPLYYRAAQIRGSEFYYSIPFSTGP--VVK 788
DB 753 salfvgskevstklftpedeasvfltdrflplyrqdashpagsvfnlrweegpesage 812
QY 789 SNVYASTSIQLDERKSPVVAAGIQMKLEFFQRKWTASQOCSLSDKCSISCODETV 848
DB 813 pmvstastavavtdkrtalaalaaagymkelfqkrfwatrtqstevdpcqcsedsl 872
QY 849 NCYLDNNQFIIIVSEDTOTGDFGFEIGEAANNKILLTMSFRRITLXYQAMCRAKES 908
DB 873 dcfvldnngflllskstrctgflgevdgavlqlismgvisqvmtydygancpksshhh 932
QY 909 DGAHGLDYPNAFISAQKIMTELVLVEFNLCS--SMHSDMTAKA-----QKLKQTL 960
DB 933 saagrpvpsiafclatrlllgelvfllewsvgsydrgeaksvfshshkhhkqdp 992
QY 961 EPCDTREYPAFVSERTIKETTGNIACEDCSKSFVIOQIPSSNLFMVYVSDSCLESVAPIT 1020
DB 993 gpcdteyrvfyvypalreaanglvcegcqkvfvgvqipnsnlllvtdptcdcsifrpvl 1052
QY 1021 MAPIEIRYNESLKERLAKQIRRRPESCHGFHPRNABECGA 1064
DB 1053 geatevkyknaavskcdmrtsqklrrtpdschafpneaqdcgga 1096

RESULT 15

ID AAY92324 standard; Protein; 1096 AA.

AC AAY92324;

DT 10-AUG-2000 (first entry)

DE Human alpha-2-delta-D polypeptide from splice variant 1.

KW alpha-2-delta-D; calcium channel; 12p13.3; gabapentin; cytosolic;

KM anticouulant; antimigrane; antiparkinsonian; antidepressant;

OS splice variant.

OS Homo sapiens.

PN WO200020450-A2.

PD 13-APR-2000.

PE 07-OCT-1999; 99WO-US23519.

PR 07-OCT-1998; 98US-0103322.

PR 30-OCT-1998; 98US-0106473.

PR 29-DEC-1998; 98US-0114088.

PA (WARN) WARNER LAMBERT CO.

PI Johns MA, Moldover B, Offord JD;

DR WPI; 2000-303744/26.

DR N-PSDB: AAA09729.

xx New human nucleic acids encoding the alpha2delta-C and alpha2delta-D

xx proteins, useful in the treatment of epilepsy, migraine, chronic pain,

xx anxiety, multiple sclerosis or cancer

xx Example 3; Page 73; 88pp; English.

xx This alpha-2-delta-D polypeptide is encoded by a splice variant that

.....

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OM protein - protein search, using sw model

Run on: August 16, 2002, 20:11:25 ; Search time 73 Seconds
(without alignments)
363.038 Million cell updates/sec

Title: US-09-787-657-5
Perfect score: 5667
Sequence: 1 MAGPGSPRRASRGASALLAA.....SLAQTVLLPLLMFSR 1085

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTOS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1148.5	20.3	1106	US-08-435-675B-5	Sequence 5, Appl1
2	1148.5	20.3	1106	US-08-336-257A-8	Sequence 8, Appl1
3	1132	20.0	1084	US-08-455-543A-56	Sequence 56, Appl1
4	1132	20.0	1084	US-08-223-305C-56	Sequence 56, Appl1
5	1131.5	20.0	1103	US-08-455-543A-53	Sequence 53, Appl1
6	1131.5	20.0	1103	US-08-223-305C-53	Sequence 53, Appl1
7	1125.5	19.9	1079	US-08-455-543A-55	Sequence 55, Appl1
8	1125.5	19.9	1079	US-08-223-305C-55	Sequence 55, Appl1
9	1122.5	19.8	1091	US-07-745-206A-25	Sequence 25, Appl1
10	1122.5	19.8	1091	US-08-455-543A-52	Sequence 52, Appl1
11	1122.5	19.8	1091	US-08-223-305C-52	Sequence 52, Appl1
12	1122.5	19.8	1091	US-08-311-363-25	Sequence 25, Appl1
13	1118.5	19.7	1091	US-08-713-118-4	Sequence 4, Appl1
14	1118.5	19.7	1091	US-09-452-007-4	Sequence 4, Appl1
15	1116	19.7	1086	US-08-455-543A-54	Sequence 54, Appl1
16	1116	19.7	1086	US-08-223-305C-54	Sequence 54, Appl1
17	1080.5	19.1	1086	5386025-8	Patient No. 5386025
18	701	12.4	508	US-08-435-675B-6	Sequence 6, Appl1
19	145.5	2.6	946	US-09-074-579-3	Sequence 3, Appl1
20	145.5	2.6	946	US-09-388-774-3	Sequence 3, Appl1
21	141.5	2.5	942	US-09-074-579-1	Sequence 1, Appl1
22	141.5	2.5	942	US-09-388-774-1	Sequence 1, Appl1
23	135.5	2.4	885	US-09-074-579-5	Sequence 5, Appl1
24	135.5	2.4	885	US-09-388-774-5	Sequence 5, Appl1
25	134	2.4	3135	US-08-323-170B-2	Sequence 2, Appl1
26	134	2.4	3135	US-08-954-441-2	Sequence 2, Appl1
27	131.5	2.3	911	US-09-074-579-4	Sequence 4, Appl1

28	131.5	2.3	911	US-09-388-774-4	Sequence 4, Appl1
29	127	2.2	2366	US-08-480-604A-10	Sequence 10, Appl1
30	127	2.2	2366	US-08-405-496A-10	Sequence 10, Appl1
31	127	2.2	2366	US-08-915-136-10	Sequence 10, Appl1
32	126.5	2.2	766	US-08-951-648-2	Sequence 2, Appl1
33	126.5	2.2	766	US-09-174-437-2	Sequence 2, Appl1
34	126.5	2.2	803	US-08-951-648-4	Sequence 4, Appl1
35	126.5	2.2	803	US-09-174-437-4	Sequence 4, Appl1
36	125.5	2.2	779	US-08-915-136-6	Sequence 6, Appl1
37	125.5	2.2	779	US-09-174-437-6	Sequence 6, Appl1
38	117	2.1	906	US-08-094-889-1	Sequence 1, Appl1
39	115.5	2.0	869	US-08-483-101-15	Sequence 15, Appl1
40	115.5	2.0	2710	US-08-480-604A-6	Sequence 6, Appl1
41	115.5	2.0	2710	US-08-405-496A-6	Sequence 6, Appl1
42	115.5	2.0	2710	US-08-915-136-6	Sequence 6, Appl1
43	114	2.0	2257	US-08-611-107-10	Sequence 10, Appl1
44	114	2.0	2257	US-08-422-560A-10	Sequence 10, Appl1
45	114	2.0	2257	US-08-468-793-10	Sequence 10, Appl1

ALIGNMENTS

RESULT 1
US-08-435-675B-5
; Sequence 5, Appl1 Application US/08435675B
; Patent No. 5710250
; GENERAL INFORMATION:
; APPLICANT: Ellis, Steven Bradley
; APPLICANT: Williams, Mark E.
; APPLICANT: Harpold, Michael Miller
; APPLICANT: Schwardt, Arnold
; APPLICANT: Brenner, Robert
; TITLE OR INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,675B
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,083
; FILING DATE: 28-SEP-1994
; APPLICATION NUMBER: US 07/914,231
; FILING DATE: 13-JUL-1992
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 08-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-53193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

FRAGMENT TYPE: Internal
US-08-435-675B-5

Query Match 20.3%: Score 1148.5; DB 1: Length 1106;
Best Local Similarity 28.5%: Pred. No. 1.5e-101;
Matches 320; Conservative 234; Mismatches 440; Indels 129; Gaps 39;

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33 SEQOIPPLV-VKLMAAFGEIKSIKAKYSGSOLLQKKYKEKEDVAIEIDLOLVK 91
25 SEPPPSAVTISWVDKMOEDLVTLAKTASGVNOLVDIYEKIODLTYVEPNNAK 84
92 AKNMEEMFKKSEAVRRLVEAEALHKEFDADL---OYEYFNAVLIINERDKGNFLE 148
85 ANDIEKLISNRKALVRLALEAEKVOAHQWREDFASNEVYVYNAK--DDLPKKNSE 142
149 GKEFT--LAPNDHFNNLPVNLSDVQVPTNMYNKDPAIVNGVYSESJANKFVNFDD 206
143 GSQIRKPVFIDANFRROVSQOHAHVHPTDIYEGSTIYLNELNMTSALDVFKKRRED 202
207 PSLINQVSGAKGFPROYPGIKMEPDE---NGVIAPDCNRKRYIOATSPKDVYTLV 263
203 PSLINQVSGATGLARYTPASPVNDNSRTPKIDLYVRRPYIDGAASPDMLILV 262
264 SGSMKGLRTIAKQVSSILDTLGDDEFNIIAYNEELHYVEPCLNGTLVQADRTNKEF 323
263 SGVSGGLTKLIRTSVSEMLETLSDDDFVNASFSNSADVS--CFQ-HLVQANVRKKVL 320
324 RHLDKLPKAGIGMDIALNEAFNLSDENNHGSGISQALMLITDQAVDTYDTIFAKY 383
321 KQAVNNITAKGITDYKKGFSFAEQLNANVSRAN--CKIIMLFDDGGEERAQELFAKY 378
384 NMPDRKRIETLYLIGREAFADNLKMMACANKGFTOISTLADVOENVEYHLVSRPV 443
379 N-KDKKVRFTSVQOHNDRCPIOMACENKGYEIEPSIGAIRINTOEYLDVGRPVY 437
444 I--DOEHVVTYEAVIDSTLDQGVMTVTVAAPVFS---KONETRSKG--TLGAVGT 496
438 LAGDKAKQVQMTNVYLDAL--ELG--LVITGLTPVENITGOFEENTNLKNQILIGVM 492
497 DVPVVELKTIPTKYKLGIGVAFATTNNGYILTHPELR-----LYEGKKRRKPNYS 550
493 DVSLEDIRLTPRFTLCPRGYFAIDPNCGYVLHPLOKPRIGVGIPITNLKRRPNVON 552
551 -----VDLSEVEMEDRDV--LRNANVRKTKG--FSMEVK---KTVDGKRLVMT 595
553 PKSOEPVTLDFDALDELNDIKYIIRKMKIDGSEKFTPTLVKSODERITIDGNRI---- 608
596 NDYVYTDIKGTPFSLGVALSRGHGYFFRGVNTIEGLHLEHPVSLADEW----- 647
609 --YVWTVPVNGTDSLALVLPYISFYIYIKAK--IETITQARYSEFTLKPDNEESGYFL 664
648 ---SYCNNTDLHEHRLHLSOLEAIKLYLKKEP--LIQCKELLOEVLFD--VVSAPLEAV 702
665 APRDYC-SDLKSDNTEFEFLNFEIDRKTNNPSCNTDLINRYLLDAGFTNELVQNVW 723
703 TSLALNKSSENSDKGEVAFAGRTGLSRINLFGAEQLTNOFLKAGDKENIFNDHPL 762
724 S-----KQKNTKGVKAFEVYTDGSTRYP-----KERGEMWQENPEYEDS 765
763 WYRAAEQIPGSEVYSIFP--STGPNKSNVNTASTSIQLDERKSPVAAVGIOMKLEF 820
766 FYKRLSDN--DNVYTFAPFNKSGGAVESGIMSKAVEIYIOGKLKPAVVGKIDVNS 823
821 FQKRWTAASRQASLDGCSISCDDETVNCTYIDNNGFIVS--EDYT-QTDDFGEIEG 877
824 WIENNTKTSIRPCAGPVDCRNSDVMDCYLLDGGFLMANHDYTNQIRFGCEIDP 883
878 AVMNKLITMGSEKRTILVDYQAMCRANKESSDGAHGLDLPY-----NAFSAVW 927
884 SLMRLLVNIISVAFNKSVDYQSVCEPGAAPKGA--GHSAYVPSIADIIQIOWMTAAW 942
928 IMTELVLFLVEF---NLCSMWHSDMTAKAOKLQLEPCDTEYPAFVSERTIKETGNI 983
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DB 943 SLIQFLSLTFPRLLLEADMEDDFTASMSK-----QSCITEQFOYFPDNDKSPFV 997
QY 984 ACEDCKSVIVIOIPSSNLFPMVYVDS--SCICEVAPITMAPIEIRYNSLKCERKAK 1041
DB 998 DGCNCRIFRIVEKLMNTNLIFFIVSESKGTCPCDT--RLIIQAEQTSDEPDCDVKOPR 1054
QY 1042 IRRRPESCHGFHEENARECGA---PSLOA---QVLLLL 1076
DB 1055 YKRGPDVCFDNNVLEDTYDCCGVSGSLNPSLMSITIGIQLVLM 1097
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RESULT 2

US-08-336-257A-8
Sequence 8, Application us/08336257A
Patent No. 5726035

GENERAL INFORMATION:

APPLICANT: Jay, Scott D
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
APPLICANT: Campbell, Kevin P.
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA

COUNTRY: USA
ZIP: 92101-2926

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336.257A
FILING DATE: 07-NOV-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 54898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0999
TELEFAX: (619) 238-0062

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-08-336-257A-8

Query Match 20.3%: Score 1148.5; DB 1: Length 1106;
Best Local Similarity 28.5%: Pred. No. 1.5e-101;
Matches 320; Conservative 235; Mismatches 439; Indels 129; Gaps 39;

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33 SEQOIPPLV-VKLMAAFGEIKSIKAKYSGSOLLQKKYKEKEDVAIEIDLOLVK 91
25 SEPPPSAVTISWVDKMOEDLVTLAKTASGVHOLVDIYEKIODLTYVEPNNAK 84
92 AKNMEEMFKKSEAVRRLVEAEALHKEFDADL---OYEYFNAVLIINERDKGNFLE 148
85 ANDIEKLISNRKALVRLALEAEKVOAHQWREDFASNEVYVYNAK--DDLPKKNSE 142
149 GKEFT--LAPNDHFNNLPVNLSDVQVPTNMYNKDPAIVNGVYSESJANKFVNFDD 206
143 GSQIRKPVFIDANFRROVSQOHAHVHPTDIYEGSTIYLNELNMTSALDVFKKRRED 202
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207 PSLIMOVYSGAKGFPROYGIKMEPDE---NGVIAFDRCNRKRYTOAASPQVYLVDV 263
203 PSLIMOVYSGATGLARYPASPBDWNSRTPKIDYVRRRWYIOGAASPDMLILVDV 262
264 SGSMKGLRLTAKOTVSSILDLDGDDFFNIJAYNEELHYVEPCINGTLVQADRNTKEHF 323
263 SGVSGLTLKLRITSVEMLETLSDDEEVNVAASFNSNQDVS-CFO-HLVQANVANKVL 320
324 REHDKLFAKIGIMDLALNAPNLSPNHTGGSGISQAIMLTLDGAVDTYDTIFAKY 383
321 KDVAANNITAKGITYDKKGSFAFEQLNMYNSRAN-CNKIMLEPTDGEERAOEIFAKY 378
384 NMPBRKVRIFTYLIGREAAFDNLKMACANKEFTOISTLADVOENMEYHVSRRPV 443
379 N-KDKKRVVFTEFSQOHNYDGRPIOMACENKGYIETIPSGAIIINIOEYIDVGRPVY 437
444 I-DOEHVDVTEAVYIDSTLDGCPVLMTVAMPFS---KONETESKG-ILLGVYGT 496
438 LAGDKAKOVQMTNMYLDAL---ELG-LVITGTLPEVFNITGOFENKTLNKLQILGVGV 492
497 DVPKELKLTIPKYLGHGAFAITNNGYILTHEPLR-----LYEGKKRRRPNTSS 550
493 DVSLEDIKRLPRFTLCNGYFFAIDPNGYVLHPNLQPKPIGVGIPINLKRKRPVON 552
551 -----VDLSEVEMEDRDV---LRNAMVNRKTG--FSMEVK---KTVDKGRVLTWT 595
553 PKSQEPYTLDLDALENDIVEINNKMITDGESGKTRTLVKSODEKIDGNRT----- 608
596 NDYVYTDIKGPPSLGVALSRGHGKYPFRGNVTIEGLHLEHPDVSIADEM----- 647
609 -YMTVPNGDYDSLALVLPYTSFYLIKAK--IEFITQAVSETLKPDPNEESGYTEL 664
648 ---SYCNNDLPRBNHLSQLEAIKILYKKEP-LLOCKELIQEYLFNA-VYSAPLEAVW 702
665 APRDYC-SDLKPSDNTEFLNMFNEFIDRKTYPNPNSCNTDLNRYLLIAGFTNELVQNW 723
703 TSLANKSENSDKGEVAFGLTRGTSRLNLFVGAEOQLNDQFLAAGHKENFADHPL 762
724 S-----KQNKIKGVKAFVYTDGITYYP-----KTAGINMOENPETIEDS 765
763 WYRRAAEQIPGSFVYSIFP--STGPRVNSNVYTAISTSOLDERSKPYVAAGIOMKLEF 820
766 FYKRSIDN--DNYVFTAYFNKSGGAYESGIMVSKAVEIYIOGKLLPAVVGIIIDVNS 823
821 FORKFWTASROCASLDGCSISCDDEVNCTYLDNNGTILVS--EDYR-QTGDFEGEIEG 877
824 WIENFTKTSIRDPCAGPYCDCKRNSDVMDCVILDDGFLMANHNDYNOIGRPFGEIDP 883
878 AVMNKLTLMGSPFKRITLYDYQAMCRANKESSDGAHGLDPY-----NAFISAVKW 927
884 SLMRHLVIAISYAFNKSTDYOSVCEPGAAPNOGA-GHRSATVPSIADILQIGWMTAAAW 942
928 IMTELVLFLVEF---NLCSWMHSDMTAKAKLQOTLEPCDTEYPAVYSERTIKETGNI 983
943 SILOQFLSLIFEPRLLEAAMEDDFTASMSK-----QSCITEQOQYFPDNSKSGFSGVL 997
994 ACEDCSKSFVIOQIPSSULFNWYVDS--SCLCESVAPITMAETIRYNESLCEPLKAK 1041
998 DCGNCSRIEHEKLEINTMLITIMESKGTCPDCT---RLIIQAEQTSJXDPDCDWVKOPR 1054
1042 IRRPESCHGFHPENARECGA---PSLOA---QTVILL 1076
1055 YRKGPDVCFDNNVLEDTYDCGVSGLNPJLWSITIGIFVLLWL 1097

APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: Mccue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 1084 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal

Query Match 20.0%; Score 1132; DB 1; Length 1084;
Best Local Similarity 28.4%; Pred. No. 5,6e-100;
Matches 322; Conservative 235; Mismatches 457; Indels 118; Gaps 41;

14 ASALLAAL-LYALAGDVRSQOIPLSV-VKLMASAFGEELKSTIAKSSGSQLQKKK 71
3 ACCLLATLTTLFOSLIGPSSSEPEPSAVTIKSWDKMQEDLVLTAKTASGVNQLDIYE 62
72 EYKDVAIIEIDGLQLVKTLAKNMEEMFHKSEAVRRLVEAAEALHKEFDADL---QY 128

3 AGCLLALTLTLFQSLIGPSSSEPPSAVTIKSWDKMOEDVTLAKTASGVNQLVDIYE 62
QY 72 EYKDVAIIEIDLOLYKRLAKNMEMFHKSEAVRLEAEALHKEPDAFL---QY 128
DB 63 KIÖDLYTEPNAROLVEJLAARDIEKLSNRKALVSLLEAEKVOAALQWREDFASNEY 122
QY 129 EYFNAVLINERDKDNFLLEKKEFI---LAPDHFNNLPVNISLSDVQVPTMYNKPDAPI 185
DB 123 VYVYNNK--DDDLPEKNDSPPSGORIKPVEIEDANRGR-QISYQHAVALIPTDIEESTIV 179
QY 166 VNGVYWSLKNVYVDNEDRDPSSLIMQYFGSAKGFROYPGIKWEPDI---NGVIAFDGR 242
DB 180 INELMWTSLADEVFFKKNREDEPSLLMOVFGSATGLARYPASPWVDNKSRTPKRIDLYDVR 239
QY 243 NKKWYIQAATSPKDVYIIVDVSGSMKGLRLTIAKQTVSSILDTLGDPPFNITAYEELH 302
DB 240 RRPWTIQQASPKDMLILDVDSGVSGLTKLIRTSVSEMLETSLDIPVNVASFNSMQ 299
QY 303 YVEPLNGTLVQADRNTKHEFHEDKLEFAKIGMLDIALNEAFNLSDFNHTQGSICS 362
DB 300 DVS-CFO-HLVQANRNNKVLKDAVANNITAKITDYKKGSFAFEQLNKNYSRAN-CN 355
QY 363 QAIMLTGADVDTYDTIEAKYMPDKRYRIETYYLIGREAPADNIKWIAACANKGFTQIS 422
DB 356 KIMLFTDGEERAOEIFKRYN-KDKKYVRFESVQOHNYERGPDIOMACENKGYEIEP 414
QY 423 TLADVOENMEVLYLSRRKYI--DOEHVYVTEAVIDSTLDDGCPVLMYVAMVFS- 479
DB 415 STGAIRINQOEYLDVLRPMVLAGDAKOVONTNYLDL---ELG--LVITGTLVFNVI 469
QY 480 ---KONETRSK--ILGVGVTVPVKELKTIPKYKLGJHYAFATNNGYIILPELRI 535
DB 470 TQGFENKTLKQOLIGVAGVDSLEDIRLPRFLCNGYFAIDPBGVYVILHNLQ- 528
QY 536 LYEBEKKRRKPNYSVDLSEVEMEDRDY-LNANAVNRTGK--FSMEVK---KTVDRG 588
DB 529 --PKNPKSQEP--VTLDFDALENDIKVEIRNNKIDGESGEKFTVXKSDERYIDKG 584
QY 589 KRVLYMTNDYTTDIKGFPSLGSVALSRGHKGYFFRGNTIEGLHDLHPDVSLADEN- 647
DB 585 NRT-----YTWTPVNGTDYSLALVLP-YSEFYIKAK--LEETIQAARYSEILKADNFE 635
QY 648 -----SYCNTDLHPEHRHLSOLEAIKLYLKKEP-LLOQDKEILOEVFLDA-VYS 695
DB 636 ESGYTFIAPROXCN-DLKISDNTEFLNENFIDRKTPNNSCANDLNRVLLDGFN 694
QY 696 ADIEAVWTSLSLANKSENSDKVEVAFGLTRTGLSRINLFGAEQLTNNDPLKAGDKENIF 755
DB 695 ELVONWYS-----KOKNIKGVKARFVVDGGITRVP-----KEAGEMWQEN 736
QY 756 NADHPPLMYRRAAEQIPGSFYVSIIP--STGPVKSNNVTASTSIOLLDEKSPVYAANG 813
DB 737 PETYEDSFEYKRSILDN-DWYVETAPFNKSGPAGESGIMVSKAIVIYQGLKLPAVVG 794
QY 814 IOMKLEFFORKFMTASROCASLDKCSISCDDETVNVCYLIDNNGFIVS--EDYT-QOTG 870
DB 795 KIIDVNSMTEINTKTSIRPCAGPVCDCRNSDVMDCVILDDGGFLMANHDDYIMQIGR 854
QY 871 FPEGIEGAVNNKLLTMGSEKRTITLYDYQAMCRANKESSDGAHGLIDFY-----NA 920
DB 855 FPEGIDPSLMRLHVNISYVAFNKSVDYQVCEBGAAPKQGA-CHRSAYVPVADILQIGM 913
QY 921 FLISAVKMITELVFLVER---NLCSMWHSMTAKAQLKOTLEPCDIETPAFVSEERI 976
DB 914 WATPAAMSLLOOFLSLTFPRLLLEAVEMEDDFTASLSK-----OSCITEQOTQYFDDNS 968
QY 977 KETTNINACEDCSKSFVIOIPSSNLFNVVVS--SCLESYAPITMAPDIETRYNSLKC 1034
DB 969 KFSFSGVLDGCGNSRIFHGKLMANTNLIPTMVESKGTCPDTRILLIQAEDTSDGP---PC 1025
QY 1035 ERLKAOKIRRRPESCHGFHPEENARECGAPSLQAOT--VLLLLPLMLUFS 1084
DB 1026 DMVKQBPYRKRGDVCFDNNVLEDYTDGCGVSGLINPMLWIIIGIQLFLMLVS 1077

RESULT 5
US-08-455-543A-53
Sequence 53, Application US/08455543A
Patent No. 5792846
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-7926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1103 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-455-543A-53

Query Match 20.0%; Score 1131.5; DB 1; Length 1103;
 Best Local Similarity 28.2%; Pred. No. 6.5e-100;
 Matches 323; Conservative 237; Mismatches 459; Indels 127; Gaps 41;

14 ASALLAAL-LYALADGVRSQOIPLSV-VKLMSAFEGEIKSTAKSSGOLLOKKK 71
 3 ACCLALATLTTLFQSLICSPSEPPSAVTKISWDKMOEDTLTKTSGVQLVDIYE 62
 72 EYKDVATEIEIGLOLVKKLAKNMEEMFKKSEAVRLVEAEALHKEFPADL--OY 128
 63 KYQDLYTEVPNNARQVEIARDEIKLSNRKALVSLALEKQVQAQWQMEDFASNEV 122
 129 EYFNAVLNERKQGNLELKEFT--LAPNDHENLDPVNISLSDVQPTNNKDPAI 185
 123 VYNNK--DDLPKERNDSPPGSGORIKPVFIEDANFGR-OISQOAHAVHPTDIESTIV 179
 186 VGVVWSESLNKVPFQNDPRLIMQVGSAGKGFROYPGIKMEDE--NGVIAFDGR 242
 180 LNELMWTSLADVEFKKNEDEPSLMOVGSATGLARYPASPWDNSTPKMTIDLYDVR 239
 243 NKKWYIQAATSPKDVYILVDVSGSMKGLRLTAKQTVSSILDTLGDDEFFNIAYNEELH 302
 240 RRPWYIOGASPKDMLILVDVSGVSGLTFLKIRTSVSEMLETLSDDDVNVASFNSNQ 299
 303 YVEPLNGTLVQADRTNKEHFEHLDKLFAKIGMLDLALNFAFNILSDPHNTGSGTCS 362
 300 DVS-CFO-HLVQANVNNKVLKDAVANNITAKGITYKKGSFAEQLLVNYSRAN--CN 355
 363 QAIMLITQCAVQVTDYTFIAKYNMPPKRVIFPYLLIGREAAFDNLKWMCAKNGFPTOS 422
 356 KIMLFTQDGERADEIFNKYN-KDKYAVREFSVGQNHYERGPLOMMCKENKGIYEIP 414
 423 TLADVOENMEYLAHLVSRKVI--DOEHVVTYAVYIDSTLTDGQPVLMYVAMPVS- 479
 415 SIGAIRINTQEVLDVLRPMVLAGDAKQVQWTVYLDAL--ELG-LVITGLTPVFI 469
 480 ---KQNEFRSK-ILGVGTDVPAVKELKTIPKYLKGHYAFAITNNGYLLHPELR 535
 470 TGQFENKTNLKNQILIGWGVDSLEDIRLTPRFLCNGYFFAIDPQVYLLHPNLOP 529
 536 ---LVEEGKKRRKPNVSS---VDLSEVEDRDRV---LRNAVNRKTKG--PS 578
 530 KPIGIGIPIINRKRPNQKSOEPTVLDLDALENDIVEIRNKKIDGSEKTR 589
 579 MEVR---KTYDKGRVLMVNDYITDKGTFPSIGVALSRGHGKYFERGAVTIEGLH 634
 590 TLVKQDERYIDKGNRT-----YMTVPYNGTDSYLVLPY-YSPYYIKAK--LEETIT 640
 635 DLEHVDVSLADEW-----SYCNTDLHPRHLSQLEAIKLYLKGERP-LLOCDK 682
 641 QARYSETLKPQNFEEGTYFTIAPRDYCN-DLKISDNTEFFLNFEIDRKTPPNPSCNA 699
 683 ELIQEVLFDA-VYSAPIEAYTSLALNKSSENDSKGEVAFGLTPTGLSINLFVGAEDLT 741
 700 DLINVLVDAGTNTLVQNTS-----KQKIKGVKARFVTTDGCITRVP----- 745
 742 NODFLKADKENIFNADHPFLWYRRAAOIPGSFYISPF--STGPVNSNVYTAISTSIO 799
 746 ---KEAGENQOENDETFEDSFYKRSLDN--DNYVFTAPYFNKSPGAVESIMVSKAVE 799
 800 LLDDEKSPVVAVGIOMLEFFQKFWTASROCASLDKCSISCDDEYVNCILINDNGTI 859
 800 IYIOGKLLKPAVAVGIKIVNSWIEFTSTISIDPCAGPVCDCRNSDWDVCLILDDGGFL 859
 860 LVS--EDYT-OTGDPEGEIEGAVNMKLLTMSFKRITLYDYQAMRANKESSDGAHGLLD 916
 860 LMANHDDTNOIGRFGELIDPSLMAHLVNIISYAFNKSVDIOSVCEPCAARQGA-GHRS 918
 917 PY-----NAFLSAVKWIMTELVLVEF---NLCSMWMDMTAKAKQLQOTLEP 962
 919 AVPSVADILQIGWMAATAAASIIQOFLSLTFPRLLLEAVEMEDDFTASLSK-----QS 973
 963 CDTEPAVSEKTIKETTGNTACEDCSKSPYIQIIPSSNLFMNVVDS--SCLCESVAPIT 1020

DB 974 CTEQTOYFFDNDKSKFSVLDGNCSTRIFHGEKLMNTLFIWESKGTCPDTRLLIO 1033
 OY 1021 MAPIEIRYNESLKCERLKQKIRRRPESCHGFPEENARECGAPSLAQOT--VILLIPL 1078
 DB 1034 AEQTSQGNP---PCDMVKOPRYRKPDPVCFDNNVLEDYDCGSGVSLNPSLWIIIGIOL 1090
 OY 1079 LMLFS 1084
 DB 1091 LMLVS 1096

RESULT 6
 US-08-223-305C-53
 Sequence 53, Application US/08223305C
 Patent No. 5851824
 GENERAL INFORMATION:
 APPLICANT: Harpold, Michael
 APPLICANT: Ellis, Steven
 APPLICANT: Williams, Mark
 APPLICANT: Feldman, Daniel
 APPLICANT: McGue, Ann
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92101-2926
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/223.305C
 FILING DATE: April 4, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/620,250
 FILING DATE: 30-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/482,384
 FILING DATE: 20-FEB-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/603,751
 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US89/01408
 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/176,899
 FILING DATE: 04-APR-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 TELEPHONE: (619)238-0999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619)238-0062
 TELEFAX: (619)238-0062
 INFORMATION FOR SEQ ID NO: 53:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1103 amino acids
 TYPE: amino acid

```

Db      860  LMANHDYTNQIGRFEGELDSLMLHLYNISYFAENKSYDQSVCEPBAAKQGA-GHRS  918
QY      917  PY-----MFLSAVKMYMTELVLVEF-----MCSWMHSDMTAKOKIKOTLEP  962
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      919  AYVPVADILQIGMWATMAANSILQOFLLSLTFPRLEFAVEMEDDQFASLSK-----QS  973
QY      963  CDTEYPAFVSEKTIKETTGNLACEDCSKSPYIQOIPSSNLMFMYVDS--SCLCSVAPIT  1020
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      974  CITEOTOYFFNDKSPFSGVLDCCGSCSRIFGHEKLMNTNLIIFIMWESGTCPCDTRLIIQ  1033
QY      1021  MAPIIRRNESJCKRKAOKRRRPESCGHFHPENARECGGAPSLQAOI--VLLIPL  1078
Db      1034  AEQJSDGPN--PCDMVKOPRRKSPDYCCFDNNVLEDDYDGGVGLNPSLWYIIGLOFL  1090
QY      1079  LLMFS  1084
          : : :
Db      1091  LLMYS  1096

RESULT  7
US-08-455-543A-55
: Sequence 55, Application US/08455543A
: Patent No. 5792846
:
: GENERAL INFORMATION:
:   APPLICANT: Harpold, Michael
:   APPLICANT: Ellis, Steven
:   APPLICANT: Williams, Mark
:   APPLICANT: Feldman, Daniel
:   APPLICANT: McQue, Ann
:   APPLICANT: Brenner, Robert
:   TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
:   TITLE OF INVENTION: METHODS
:   NUMBER OF SEQUENCES: 57
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: Brown, Martin, Haller & McClain
:     STREET: 1660 Union Street
:     CITY: San Diego
:     STATE: California
:     COUNTRY: USA
:     ZIP: 92101-2926
:
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Diskette
:   COMPUTER: IBM Compatible
:   OPERATING SYSTEM: DOS
:   SOFTWARE: FastSEQ Version 1.5
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/08/455,543A
:     FILING DATE: May 31, 1995
:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: 08/223,305
:       FILING DATE: April 4, 1994
:       PRIOR APPLICATION DATA:
:         APPLICATION NUMBER: 07/868,354
:         FILING DATE: April 10, 1992
:         PRIOR APPLICATION DATA:
:           APPLICATION NUMBER: US 07/745,206
:           FILING DATE: 15-AUG-1991
:           PRIOR APPLICATION DATA:
:             APPLICATION NUMBER: US 07/620,250
:             FILING DATE: 30-NOV-1990
:             PRIOR APPLICATION DATA:
:               APPLICATION NUMBER: US 07/482,384
:               FILING DATE: 20-FEB-1990
:               PRIOR APPLICATION DATA:
:                 APPLICATION NUMBER: US 07/603,751
:                 FILING DATE: 04-APR-1989
:                 PRIOR APPLICATION DATA:
:                   APPLICATION NUMBER: WO PCT/US89/01408
:                   FILING DATE: 04-APR-1989
:                   PRIOR APPLICATION NUMBER: US 07/176,899
:                   FILING DATE: 04-APR-1988
:                   ATTORNEY/AGENT INFORMATION:

```



```

APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-223-305C-55

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Query Match      19.9% Score 1125.5; DB 2; Length 1079;
Best Local Similarity 28.4%; Pred. No. 2.4e-99;
Matches 321; Conservative 234; Mismatches 454; Incls 123; Gaps 41;

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OY 14 ASALLAAL-LYAALGDVRSPOQIPLSV-YKLMAAFGEIKSIAAKYSGSOLLQKKYK 71
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 3 AGCLLALTLTFLQSLILIPSSSEPPSAVTTKSWDKMOEDLVTLAKTASGVNQLVDIYE 62
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 72 EYKDVAAIEIDGLQVLKAKMEEMFKKSEAVRLVEAAEAAHKEFDADL--OY 128
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 63 KYODLYTEPNNAQLVEIAARDIEKLKLSNRKALVSLALEKQVQAHHQMEDPASNV 122
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 129 EYFNALVINEKDKGNFLELKEFT---LAPDHENNLCPNISLSDCVPTMYNKDPAI 185
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 123 VYNAK--DDLDPEKNDEPSQRIKPVFIEDANFGR-OISYQHAHVPIDYEGSTIV 179
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 186 VNGVWSESLKNEFVNDPDSLIWOYFGSAKGFEROYPGIKWEPDI--NGVLAFOOR 242
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 180 LNEIWTALDEVEFKKNEEDPSLMOYFGSAYGLARYIPASPWDNKRTPPKIDLYDVR 239
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 243 NRKWTQATSPKDVILVDSGSKGLRLTAKQVSSILDTLDDDFENIAYNEELH 302
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 240 RRPWTQGAASPKDMLIVDSGVSGLKLRITSVSEMETLSDDIPEVNVASFNSMQ 299
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 303 YVEPLNGLTVQADRTNKEHREHLDKLFAGCIGMLDIALNAFENILDFNHTGSGTCS 362
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 300 DVS-CFO-HLVOANVRNKKVLLKDAVNNITAKGTDYKKGFSAFQQLNYNVSRRAN-CN 355
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 363 QAIMLTGAVDYDTIFAKYKMWPRKRYIFTYLIGREAFADNLKMWACANKGFPTOS 422
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 356 KIIMLTGGEERAOEITNNKIN-KDKKRVRFESVGOHNHYERGPIOMNACENKGYEIEP 414
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 423 TLADVOENMEXLHVLSPRYKI--DOEHNVWTEAYIDSTLTDGQPVLMTVAMPVES- 479
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 415 SIGAIRINTQOELVDLGRPVYLAGDKAKOVQWNTNYLDAL--ELG- LVITGILPVFNI 469
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 480 ---KONETRSKG-IILGVGVDVYKELIKTIPKTKLIGHGAPAITNNGYLLHPELRL 535
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 470 TGOEFKNTLNQLITLGVGVDVSLIEDIKRLPRFLCPNGYFFAIDPNGVYLLHPNL-- 527
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 536 LYEECKRRKRRPNYSVDSEVEMEDRDV-LRNAMVNRKTGK--FSMEYK----KTVDG 588
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 528 -----QKREP-VTLDDLDALENDIVELRNKMDIGSGSKTFTYVKSODERIDG 579
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 589 KRLVMTNDYVYTDIKTFPSLGVALSRGHGKFFPRGNVTIEGLHDEHPDVSLADEW- 647
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 580 NRT-----YMTVPNGIDYSLALVLP-YSFYIYIKAK--LEETITQARYSTLAKPDNE 630
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 648 -----SYCNTDLHPERHLSQLEAIKLYLKGEK-LIQCKEGLQEVLEDA-VVS 695
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 631 ESGYTFIAPRDYCN-DKLTISDNTEFLNPFNEFIDRKTPPNNSCADLNRVLLDAGFTN 689
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 696 APIEAYWTSIALNKSENSDKVEVAFGLTRGSLSRINLFGVAGQJLNQDFLAKGKENIF 755
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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DB 690 ELVQNTWS-----KOKNKGVARFVYTDGITTIRYP-----KEAGEWQEN 731
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OY 756 MADHPELWYRRAEQIPGSEFVYSIF--STGPVYKSNVYVASTIQLDERSPVVAAYG 813
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 732 PEYEDSFYKRSIDN--DNVETLAPYFNKSGPCAYESGIMVSKAIEYIQGKLKPAVVG 789
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 814 IQMKLEFFQKRWYASRQASLDGKCSISCDDETVCYILDNNGFLVYS--EDYT-QTGD 870
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 790 IKIDVSWIENFTKTSIRPDCAGPYCDCKRNSDVMCVILDDGFLMANHDDYTMOIGR 849
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 871 FPEGIGAVNNKLTLMGSKRITLYDYQAMCRANKRESSGAGHLDPPY-----NA 920
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 850 FPEGIDPSLMRLHVNISYVAFNKSIDYOSYCEGGAAPKQGA-GHRAYVPVADIIQIGW 908
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 921 FLSAVWMITELVFLVEF---NLCSMWSMTATAKAOKRLQTLPECDTEYPAFVSERTI 976
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 909 WATAAAMSTIQFLSLTFPRLLLEAVEMEDDPTASTLSK-----QSCITEQYQYFDNDS 963
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 977 KETGINIACEDSKSFVIOQIPSSNLFMYVDS--SCLESVAPITMAPIEIRYNESLKG 1034
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 964 KFSFGLDGCNCSRIFHGEKLMNTLIFLWVESKGTCPDTRLILQAEQTSDEGN--PC 1020
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1035 ERLKAKIRRPESCHGFPEENARECGAPSLQAOQ--VLLLPPLMLDFS 1084
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1021 DWVKOPRYKRGDVCYCDNNVLEDYTDGCGVSGLSLWYIIIGIQLLMLYS 1072
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 9
US-07-745-206A-25
Sequence 25, Application US/07745206A
Patent No. 5429921
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: McGue, Ann
APPLICANT: Feldman, Daniel
TITLE OF INVENTION: Human Calcium Channel Compositions and
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: Fitch, Even, Tabin & Flannery
STREET: 135 S. LaSalle
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,206A
FILING DATE: 19910815
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B
REFERENCE/DOCKET NUMBER: 51504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-745-206A-25
Query Match      19.8% Score 1122.5; DB 1; Length 1091;
Best Local Similarity 28.4%; Pred. No. 4.7e-99;

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	Matches	323: Conservative	233: Mismatches	460: Indels	121: Gaps	41
OY	14	ASALLAAL-LYALGCDYRSBOQIPLSY-VLWMSAFGEETKSIATAKSGSOLLQKKK	71			
Db	3	AGCLLATLTLTPOSLIGPSSSEPPSAVTIISWDMKMOEDLVTLTKTASGVOLVDIE	62			
OY	72	EKKVAVTEIDGLTVKKLAKNMEMPHKKSSEAVRLEAALDEALHKEPADI---	OY 128			
Db	63	KQODLYTEPNNAKQVLELAARDIEKLSSNRKALSLLEAEKQAOAHQMRDEAFSNEY	122			
OY	129	EYFNALINERKDKGNFLELGEFT--LAARDHFNLPVNITSLSDVPQPTMYNKPDAI	185			
Db	123	VYNNK--DDLDPEKNDSPPSQRIKPVIEDANGR-QISYQHAVALHTPIIYESTIV	179			
OY	186	VAGVYMSLANKYEVNEDRDPSLIMQVFSKAKGFROYGKIEWDE--NGVIAFDCR	242			
Db	180	LNELMWTSAIDDEVFKNREDEPSLLMOVFSATGLARYPASPWNDSRTPKIDLYDVR	239			
OY	243	NKKWITQAAATSKDQVITLVDSGSKGLRLTAKQTVSSIDTLGDDDFNITAYEELH	302			
Db	240	RRPWTIQGASRKMDILVDVSGVSGTLKILRTVSEMLETLSDDDVNVASFNSMQ	299			
OY	303	YEPCLNGLTQADRTNKEFHREHDLKLPKACIGMDILNAFNLISPFNTQGSIS	362			
Db	300	DVS-CFO-HLVQANRNKKVLDKDVANNITAKITDYKKSFSAFEDLLNYSNAN--CN	355			
OY	363	QAIMLITDCAVDYDTITFAKYNMPDKRYRIPTYLIGREAFADNLKMAKANKGFTQIS	422			
Db	356	KIMLTDFGGEERAQEIFKNYN-KKKVAVFFRSVQHNHYERGPLOMACEKNGYEIEP	414			
OY	423	TLADVOENMEYLAHLSRPKYI--DOEHVYVTEAVIDSTLDDGQPVLMTYAMVES-	479			
Db	415	SIGAIRINQOEVLVDLGRPMVLAGKAKAOVQNTNYLAL--ELG--LVITGTLPEVNI	469			
OY	480	---KONETRSK--ILGVVGTDPVPKELKLTIPKXKILGHVAFATNNGYILTHPELR	535			
Db	470	TGQFENKTRNLKQDILLGVGVDSLEEDIKRLTRPTLCNGYIEFADIPNGYVLLHNPLO-	528			
OY	536	LYEECKRRKRRPNYSVDLSEVEMEDRDV-LRNAVNRKTGK--ESMEVK---KTVDGK	588			
Db	529	--PKPKSQEP--VTLDFLAELENDIKVEIKNMKIDGSGKTRTLVKSDDERIDKG	584			
OY	589	KRVLYMTNDYITTDIKGPFSLGVALSRGHGKYF-----RGVNTIEBGL-	633			
Db	585	NKT-----YTWTPNGDYSIALVLPY-YSFYVIKAKLEETITQARSKKGMKSEYTK	637			
OY	634	-HDLEHPVSLADEMSYCTDLHPRHLSOLEAIKIVKGEK-LLQDCKDLQIEVLFD	691			
Db	638	PDNFEESEGYTFAPADYCH-DLKITDNNTEFLNFNEFDRTKTPNNPSCNADLINRVLD	696			
OY	692	A-VVSAPITEAVYTSIALNKSSENSDKVEVAFLGTRTGLSRIMLFVGAEOULTMODELKAD	750			
Db	697	AGFTMELQVWYS-----KQKNIGGVARFVYTOGGITRYVP-----KEAGE	738			
OY	751	KENITNADHFLMYRAAEQIDGFSVYSLP--STGPVKNKSNVYVASTISIQLDERKSPV	808			
Db	739	NWOENPETYEVSFYKRSLDN--DNVYFAPYFNKSGPGAESGIMVSKAVETIYQIKLK	796			
OY	809	VAAVSIQKLEEFQOKKPYMASRQCSLDGKGISODDELYNCLYLDNNGFIIVS--EOT	866			
Db	797	PAYVGIKIDVNSWIEFTKTSIRDPACAGVCCCKRNSDVMDCVILDDGGFLLMANHDDY	856			
OY	867	-QTQDFGEIEGAVYNNKLITMGSFKRITLYDVQACRANKESSDAHGILDPY-----	918			
Db	857	NQIGFFAEIDPSLRLHLVNISYVAFNKSSTDQVSCCEGGAAPKQGA-GHRSAYVSVADI	915			
OY	919	---NAFLSAVKIMTELVLVEF---NLCSMWHSMDTAKAQKLTLEPCDTEYPAFV	971			
Db	916	LOIGMMAATAAAMSILQOELLSTLTPRLLLEAVEMEDDDFASLSK-----QSCITROTGYF	970			
OY	972	SERTIKETTGNIACDCKSPYIQOIPSSNLFMVVYDS--SLCDSVAPITMAPIEIKRN	1029			
Db	971	FDNDKSFSSGVLDGCSGRIFGKELMTNMTLFIWESGTCPCDTRLLIOAEQTSQDGN	1030			

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10
10030 ESKCEBTLKQKQKIRRESQHGHEPNEARECGGASLQAGT--VLLLEPLLMFMS 1084
10131 ---PCDMVKQPRRRKRGPFVCFDNNVLEDTYDCGGVSGLPSLMYTIIGIOLFLLMLVS 1084
10131 ---PCDMVKQPRRRKRGPFVCFDNNVLEDTYDCGGVSGLPSLMYTIIGIOLFLLMLVS 1084

RESULT 10
US-08-455-543A-52
Sequence 52, Application US/08455543A
Patent No. 5792846
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

```

FRAGMENT TYPE: internal
US-08-455-543A-52

Query Match 19.8%; Score 1122.5; DB 1; Length 1091;
Best Local Similarity 28.4%; Pred. No. 4.7e-99;
Matches 323; Conservative 233; Mismatches 460; Incls 121; Gaps 41;

14 ASALLAAL-LYALAGDVRSQQIPLSV-VKLASAFGEFKLSIAAKYSSQLLOKKK 71
3 AGCLLATLTLFQSLIGPSSSEPPSAVTIKSWDKMQEDELVTAKIASGNOVLDTYE 62
72 EYKQDAIEEIDQLQVYKLAKNMEEFHKKSEAVRRLVEAEHRLKHEFDADL---QY 128
63 KYQDLYTEPNNARQVLVIAARDIKLSNSKALVALALEEKYQAAHOMEDPASNEV 122
129 EYPAVLINERDKGNLELKEFT--LAPNHPNNLPVNISLSDVQVPTMYNKPDAI 185
123 VYNNAK--DDIDPEKNDSEPGSQRIKPVFIEDANFGR-QISYQAAVHIPDIYEGSTIV 179
186 VNGVYMSLKNKVPYDNDRPSLIMQYFGSAKGFROYPGIKMEPD---NGVIAFDGR 242
180 LNEIWMTSALDEVEFKKNEEPPSLIMQYFGSATGLARYPASPMVDNERTPKIDLYDVR 239
243 NRKWIQAATSPKDVVILVDVSGSMKGLRLTAKOTVSSIIDLTDGDPENFIAYNEELH 302
240 RRPWYIOGAASPKMILVDVSGVSGTLKILRTSVSEMLETISDDIFVNVASRNSNAQ 299
303 YVEPLNGLTVOADRTNKEHREHLDKLPAKGIGMLDIALNEAFNILIDFNHTGOGSICS 362
300 DVS-CFQ-HLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAEQLLINYNSRAN-CN 355
363 QAIMLITGADVITYTTIAKINMPKRYRIETYLIGREAFADNLIKMAIACANKGFTQIS 422
356 KIMLFTDGGERAQELINKNY-KDKKRVFERSVGOHNTERGPOMIACEKNGYYEIP 414
423 TLADQENMEXELVLSRPKYI--DOEHNVWTEAYIDSTLDDOGPVLMTVAPVES- 479
415 SIGARITQOELVDVLRPMVLAGKAQOVONTNYLDL---ELG--LVITGTLPEVNI 469
480 ---KONETRSKG-ILGVGTDVPVKELIKTIPKYLIGHYAFATINNGYILTHPELRL 535
470 TGOFEKNKTLNKLQILGVGVDVSLIEDIKRLPRFTLCPNGYFAIDPVGYYLHPNIG- 528
536 LYEBCKRRKRRNYSVDLSEVEMEDRDV-LRNAMVNRKTGR-FSMYK---KTVDKG 588
529 --PKNPKSOEP-VTLDELDALELNDIVEIIRNMKIDGSEKTERTYVKSODERYIDG 584
589 KRVLMTNDYTYTDIKGTPFSIGVALSRGHGKYF-----RGNVTEEBGL- 633
585 NRT-----YWTVPVNGTDYSLALVLP-YSFYTIKALEETITQARSKKGMKSEITLK 637
634 -HDLHPDVSLADEWSYCNLTLHPEHRLSOLEAIKLYLKGEK-LLAQCKELIOEVLFD 691
638 PDNFEESGYTFLAPDYCN-DLKISDNNTFELNNEFIDRKTPNPNPCONADLINRVLLD 696
692 A-VVSAPLEAVTSLALKSENSDKGVAVPLGTGTGSRINLFGAQLTQODLLKAGD 750
697 AGFTNELVQONWS-----KQKNIGVAKARFVVTGGITRYV-----KEAE 738
751 KENIFNADHPFLMYRAAEQIPGSFVYSIPF-STGPVNKSNVVAVASISLOLDEKSPV 808
739 NMQENPETEEDSFYKRSIDN--DNVYFAPYFNKSGPGAYESGIAVSKAVELYIOGKLK 796
809 VAAVGIOKLEFFORKEFTASRQCSISDDETVNICYLIDNNGFIVLS--EDYT 866
797 PAVYGIKIDVSMIENFTKTSIRDCAGPVCCKRNSDVMDCVILDDJGFFLLAMHNDYT 856
867 -QTGFEEIEGAVYNNKLLTMGSFKRITLYIQAMCRANKESDGAHGLIDPY----- 918
857 NOIGFFFEIDPSLMRLVNIISVAFNKSYDQVSCGGAAPKGA-GHRSAYVPSVADI 915
919 ---NAFISAVKIMTELVLVEF---NLCSWHSMDMTAKAQKQLTLEPCDTEVPAY 971

DB 916 LQIGWATATAAASIIQQFLLSLTFPRLLAEVEMEDDFTASLSK-----QSCITEQTYF 970
QY 972 SEBTIKETGNIACEDCSKSEFVYIQIIPSSNLEPMVAVDS--SCICESVADITMAPIEIRN 1029
DB 971 FNDSSFSFGVLDGCGNCSIRFHEKELMTNLIJFIMVESKGTGCPCDRLILOAEQTSDCPN 1030
QY 1030 ESLSKCERLAKQIRRRPECHGFHPEENARECGGASLQAT--VLLLPILLMLFS 1084
DB 1031 ---PCDMVAKQPIRKGPDVCCFDNNVLEDYTDGCGVSGLNPSIMYIIGIOFLLLMLVS 1084
RESULT 11
US-08-223-305C-52
Sequence 52, Application US/08223305C
Patent No. 5851824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Reidman, Daniel
APPLICANT: McCue, Ann
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Hallier & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-223-305C-52

Query Match 19.8%; Score 1122.5; DB 2; Length 1091;
Best Local Similarity 28.4%; Pred. No. 4,76-99;
Matches 323; Conservative 233; Mismatches 460; Indels 121; Gaps 41;

14 ASALLAAL-LYALGADVRSQQIPLSV-VKLMSAFGGEIKSIAAKYSQQLQKKYK 71
3 AGCLLALTLTLFQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDIYE 62
72 EYKDVAAIEELDIGQLVYKLLKNMEEMFHKKSEAVRRLVEAEAHKLHEFDADL---QY 128
63 KYODLYVEPPNNAKOLVIAARLDEIKLSNRSKALVSLALEAEKQAAHQMREDFASNEV 122
129 EYFNAVLINERDKDNLELGEFT---LAPNDHFNLPVNISLSDVOPTNMYNKKDPAI 185
123 VYVNAK---DLDLPEKNDSEPSQRIKPFIEDANGR-QISYQHAHAIHPDIYEGSTIV 179
186 VNGYVSSSLKKVVDNDRPSLIWQYFGSAKGFROYPGIKPEPDE---NGVIAFCR 242
180 LNELNMTSALDEVERKKNREEDPSLIWQYFGSATGLARYPASPVWDNSTRPKIDLYDVR 239
243 NRKVTIQATSPKDVILIVDVGSMKGLRTIAKOTVSSILDTIGDDFFNIIAYNEELH 302
240 RRPVYIGGAASPKMMLIVDVGSGVSLTLKIRTSVSEMLETSLDDDFVYVASNSMAQ 299
303 YVEPCLNCTLVQADRTNKEHREHLDKLEAKGIMLADIALNEAFNISLDFNHTGGSTICS 362
300 DVS-CFO-HLVQAVNRKKVLLDAVNNTAKITDYKKGFSFAEQLLNVYSRAN--CN 355
363 QAILIITDGAANDTYDTYFAKNMPDRKRIITYLLIGRAAANLNKMAWCAKNGFTQIS 422
356 KIMLFTDGGGERAOEYFNKN-KDKKAVREFSOGHNYERGPLOMAWACEKGGYYTIP 414
423 TLADVOENMVEYLVLSHPKYI---DOEHVVMTEAYIDSTLTDGCPVLTMTVAPVES- 479
415 SIGAIRINTQGYLDVIGRPVYLADKAKQVOMTVYLDAL---ELG--LVITIGLIPVNI 469
480 ---KONETRSKG-ILGAVGTDVPVKELKTIPIYKLGIGHYAPAITNGYIILHPELRL 535
470 TGOENKRTNLKNOQLIGVGVDSLEIDIKRLTPRETLCPNGYFAIDPENGVLHPNLQ- 528
536 LYEGSKRRKRNYSVDSLEVEMEDRDVY-LRNAMVNRKTKG--FSMEVK---KTVDKG 588
529 --PNPKSQEP-VTLDFLDALELNDIKVETIRNMKIDEGSEKTFRTLVKSODEERYIDKG 584
589 KRVLMTNDYVYTDIKGTFEIGVALSRGHGKYF-----RGNVTIEEGL- 633
585 NRT-----YMTFVNGTIDYSLALVLPY-YSFYIKAKLEETITQARSKKKMKMDSFLK 637
634 -HDLHPDVSLADEWSTCNDLAPHRHLSQLAIKLYLKEKP-LLOCKDELIQEVLPD 691
638 PDNFEESGYTFIAPRDYCN-DLKISDNNTFEFLNPFNEFIDRKTNNPCNADLIRVLLD 696
692 A-VVSAPIEAFTSLALNKSNSDKGVEAVFLGRTGSRINLFGAQLNODFLAKGD 750
697 AGFTNELVQNTWS-----KKNIKGVAKARFVVDGITTRYP-----KEAGE 738
751 KENIFNADHFLMYRAAEQIDGSEFVYSIP--STGPVKNKNVYASTSIOLDERKSPV 808
739 NMGNPPEYEDSEFYKRLSDN--DNVYTFAPYFNKSGGAYISGLIMVSAVAEYIYQKILK 796
809 VAAVGIMKLEEFQKRTKWTASRQCASLDGKCSISCDDETVNVCYLLDNGGFLVVS--EDYT 866
797 PAVVGFIDVMSIENFTKTSIRDPACAPVDCDKRNSDVMDCVILDDGFLIMNHDDYT 856
867 -QTDVDFGEIEGAVMNKLLTMGSEFKRITLYQAMCRANKSESSDGAHGLDPY----- 918

DB 857 NOIGRFEIEIDPSLMRHLVNISVYAFNKSVDYQSVCEPGAAPKOGA-CHRSAYVPSVADI 915
QY 919 --NAFLSAVKWIMTELVLIVEF-----NLCSWMHSDMTAKAKLQTLLEPCDREYPAFV 971
DB 916 LQIGMMATTAAMSLIQGLLSITFPRLLEAVEMEDDDFTASLSK-----QSCITPQTYF 970
QY 972 SERTIKETTGNIACEDSKSFYIQIIPSSNLFMVVDS--SCLESVAPITMAPIEIRYN 1029
DB 971 FDNDSKSFSGVLDCGNCGRIFGEIKLMTNLIIFIVESEKGTCPDTRLIIQAEGTSDGPN 1030
QY 1030 ESLKCEERKAKIRRRPSCCHGFHEENARECGAPSLQAQT--VLLLLPILIMFVS 1084
DB 1031 ---PCDMVKQPYRRKGPVCEFDNNVLEDYTDGGSGLNPSLWYIIGIQLLWLVS 1084

RESULT 12

US-08-311-363-25
Sequence 25, Application US/08311363
Patent No. 5876958

GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,363

FILING DATE:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206

FILING DATE: 15-AUG-1991

ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-51506

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999

TELEFAX: (619)238-0062

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 1091 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-311-363-25

Query Match 19.8%; Score 1122.5; DB 2; Length 1091;
Best Local Similarity 28.4%; Pred. No. 4,76-99;
Matches 323; Conservative 233; Mismatches 460; Indels 121; Gaps 41;

14 ASALLAAL-LYALGADVRSQQIPLSV-VKLMSAFGGEIKSIAAKYSQQLQKKYK 71
3 AGCLLALTLTLFQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDIYE 62
72 EYKDVAAIEELDIGQLVYKLLKNMEEMFHKKSEAVRRLVEAEAHKLHEFDADL---QY 128

Db 63 KYODLYTEVPNNAROLVETIARDIEKLLSNRSKALVSLALEAKVOAHHQWREDFASNEV 122
QY 129 EYFNNAVLIERNKDGNFLELGEFT---LAPDNHFNLPVNISLSVYVPTNMYNKDPAL 185
Db 123 VYYNNAK--DOLPEKNDSEPGSORIKPVEITEDANFGR-QISYOAHAHVHPTDIYEGSTIV 179
QY 186 VNGVYSESLNKVYDNFDRPSLIWQYFGSAKGFROYPGIKWEDE---NGVIAFDOR 242
Db 180 LNELMNTSALDEVFKNKREDEPSLIWQYFGSAGTLARYPASPVWVNSRTPNKIDLYDVR 239
QY 243 NRKWTIOAATSPKDVVILVNVSGSMKGLRTLITAKOTVSSILDTLGDDEFFNIITAYNEELH 302
Db 240 RRPVYIOGAASPKDMLILVDVSGVSGTLKLRITSVSEMLETLSDDDPVNVAASFNSMQ 299
QY 303 YVEPCLNGTLVQADRTNKHFRHLDKLEPAKIGIMDLALNEAFNITLSDPNHTGOGSICS 362
Db 300 DVS-CFQ-HLVQANVRNKKVLDVANNITAKITDYKKGFSAFEBOLLNMYNSRAN--CN 355
QY 363 QAIMLITDGAVDYDTIFAKYNNMPDRKVRIFTYLIGREAAFDNLKMACANKGFTQIS 422
Db 356 KIMLFTDGGERRAQEIFNKYN-KDKKVYVFRFVSGOHNYERGIOMMACENKGYIYEIP 414
QY 423 TLADVOENMEYLHVLSPRKVI--DOEHNVWTEAYIDSTLTDDGQPVLTMTVAMFVS- 479
Db 415 SIGAIRINTQETLDVLRGMVLAGDKAKQVMTNVDLAL---ELG-LVITGTLVFN 469
QY 480 ---KONETRSK--ILGVGTVPVKELKITPKYKLGHGAFAITNNGYIITHEBLR 535
Db 470 TGOFEKRTMLKQOLILGVGVSVSEDIKRLTPRFLCPNGYFAIDPBGYVLHFNLO- 528
QY 536 LYEEGKRRKPKVSVSDVSEVEMEDRDY-LRNAVNRKTGK--FSMEYK---KIVDVG 588
Db 529 ---PKNPKSOP--VITDFDALENDIKVEIRNKMIDGESGKTEFTLVKSDERITDG 584
QY 589 KRVLVMTNDYVYTDIKGTPSLGVALSRGHGYFF-----RGVYTIIEGL- 633
Db 585 NRT-----YMTVPVNGTDYSLALVLP-YSPFYIKAKLEERTITQARSKKKMKKDESLIK 637
QY 634 -HDLHPVSLADENSYCTDLHPEHRHLSQLEAIKLYLKKEP-LLJCDKELIQEVL 691
Db 638 PDNFEESGYTFTIAPRDYCN-DKISDNNTFELNFEFTIDRKTPNPNPSONADINRVLLD 696
QY 692 A--VVSAPVAYWTLALNKSSENSDKGEVAFLGTGTGLRINLFGVABEOLTDNQDFLAKAG 750
Db 697 AFTFHELVONYMS-----KOKNIKGVKARFVYTDGCTITRVF-----KEAGE 738
QY 751 KENIFNADHFLMYRRABQIPGSPYISIPF--STGPRVKSNNVYASTSITOLDERRKSPV 808
Db 739 MNQENPEYEDSFYKRSIDN--DNYVFTAPYFNKSGPGAYESGIMVSKAVEIITQGLKLK 796
QY 809 VAAVGIOAKLEFFORKEFTWASROCASLDGKCSISCDDEFVNCYLIDNGFILVS--EDYT 866
Db 797 PAVVGKIDVNSMIENFTTTSIRDPGAPVCCCKRNSDVMDCVILDDGFFLLMANHNDYT 856
QY 867 -OTGDFEGIEGAVNNKILTMGSFKRITLYDOAMRANKESDGAHGLDVP----- 918
Db 857 NOIGRFFGIDPSLMHNLNIVYAFNKSIDYQSCPEGAAPRKGA-GHRSAPVPSVADI 915
QY 919 ---NAFLSAVKIMTELVLVEF---MLCSNMHSDMTAKAKOIKCTLEPCDTEYPAFV 971
Db 916 LQIGMMATTAASIIQOFLSLTLFPRLLAVEMEDDDFTASLSK-----QSCITTEQYF 970
QY 972 SERTIKETTGNIACEDCSSEYVIOQIPSSNLMVNVDS--SCLCESVAPITMAPIRNV 1029
Db 971 FNDSPFSFGVLDGNCSCSIFHGEKLMNTNLFIWESKGTCPDCDFLLIOAEPOTS DGN 1030
QY 1030 ESLKCRSLAKOIKIRRPESCHGFHPEENARECGAPSLAQOT--VTLLPLILMMS 1084
Db 1031 ---PCDMVQAPRYKRKGPVDCFDNNVLEDYTDGCGVSGLNPBSLMTYITIGIQLMILVS 1084

RESULT 13
US-08-713-118-4

Sequence 4, Application US/08713118
Patent No. 6040436
GENERAL INFORMATION:
APPLICANT: Franco, Rodrigo
APPLICANT: Sun Chen, Ai Ru
APPLICANT: Sney, David J.
TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
NUMBER OF INVENTION: CALCIUM CHANNEL SUBUNITS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P. C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,118
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mata, Elizabeth W.
REGISTRATION NUMBER: 38,236
REFERENCE/DOCKET NUMBER: ACC96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
TOPOLOGY: 1linear
MOLECULE TYPE: protein
US-08-713-118-4
Query Match 19.7%; Score 1118.5; DB 3; Length 1091;
Best local Similarity 28.4%; Pred. No. 1.2e-98;
Matches 323; Conservative 222; Mismatches 461; Indels 121; Gaps 41;
QY 14 ASALLAAL-LVYALGDVRSQOIPLSV-VKLMSAFGEIKSIAKYSGSOLLQKKY 71
Db 3 AGLLALTLFLFSLILGSPSEPPPSAVITKSMVDMQMDLVTLAKTAGVNOVDIYE 62
QY 72 EYEKDAVIEIDLOLYKTKAKNMEEMFKKSEAVRRLVAAEBAHLKHEFDADL---QY 128
Db 63 KYODLYTEVPNNAROLVETIARDIEKLLSNRSKALVSLALEAKVOAHHQWREDFASNEV 122
QY 129 EYFNNAVLIERNKDGNFLELGEFT---LAPDNHFNLPVNISLSVYVPTNMYNKDPAL 185
Db 123 VYYNNAK--DOLPEKNDSEPGSORIKPVEITEDANFGR-QISYOAHAHVHPTDIYEGSTIV 179
QY 186 VNGVYSESLNKVYDNFDRPSLIWQYFGSAGGFROYPGIKWEDE---NGVIAFDOR 242
Db 180 LNELMNTSALDEVFKNKREDEPSLIWQYFGSAGTLARYPASPVWVNSRTPNKIDLYDVR 239
QY 243 NRKWTIOAATSPKDVVILVNVSGSMKGLRTLITAKOTVSSILDTLGDDEFFNIITAYNEELH 302
Db 240 RRPVYIOGAASPKDMLILVDVSGVSGTLKLRITSVSEMLETLSDDDPVNVAASFNSMQ 299
QY 303 YVEPCLNGTLVQADRTNKHFRHLDKLEPAKIGIMDLALNEAFNITLSDPNHTGOGSICS 362
Db 300 DVS-CFQ-HLVQANVRNKKVLDVANNITAKITDYKKGFSAFEBOLLNMYNSRAN--CN 355
QY 363 QAIMLITDGAVDYDTIFAKYNNMPDRKVRIFTYLIGREAAFDNLKMACANKGFTQIS 422
Db 356 KIMLFTDGGERRAQEIFNKYN-KDKKVYVFRFVSGOHNYERGIOMMACENKGYIYEIP 414

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0Y 423 TLADQVEMVLEHVLSPPKYI--DOEHDIYVFAVYDSLTLDDQGVMTVTWAMVFS- 473
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Db 415 SIGAIRITQETLVDLGHPRVLADCKAKQOMTVNYDAL---ELG--LVITGTLPEFNI 469
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 480 ---KONETRSGK-TLLGVGSTDVBPVELLTIPIPKYLGIGVAFALTNNGYLITPEBLR 535
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 470 TGFQFENKTNLKNOLILGVGVADVSLDEDIKRLTRPFTLCPRGYFALDPNVATLHNNLG- 528
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 536 LYEBAKRRKRKNYSSVDSLEVEMEDRDVY-LRNAAVNRKTKG--FSKVEG---KTVDKG 588
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 529 --PKNPKSQEP--VTLDFLDALELENDIKVELIRNMIMIDEGSEKFTFRLVKSODERYIDKG 584
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 589 KRLVMTNDYUYYTIDIKGPPSLGVALSRGKXYE-----RGNTIEGL- 633
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 565 NRT-----YMTVPNGTIDSLAVLTP--FSFYIAKLEETTOARSKKGNKDKSETLK 637
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 634 -HDEHPDVSLEADMSYCNTDHPHEHNLSQLAIKLYLKGEP-LLOCDKELIQEVLDP 691
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Db 638 PDNFEESEGYTLARDCYN-DLKTSDNNTPELLNFNFIDRKTPNPNPCMAADLNNVLDD 696
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0Y 662 A-VVSAPLEAVTSLALNKSNSDKGYEVAFLGTRGLSRINLFPVGAEOULTNODFLKAD 750
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Db 697 AGFTNELVQNYMS-----KKNIKGVKARFVYTDGITRVP-----KEAGE 738
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 751 KENIFNDHPFLVBRRAEQLPGSEFVYSIFP--STGVNKSNNVYASTSLOLDEKSV 808
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 739 NMQENPETYEDSFYKRSLDN--DMYVETAPYFNKSGVAYESSIMVSKAEYIYQKLLK 796
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 809 VAAVGIOMKLEFPORKEFWTSRQCSALDGCISCDDETVNCTYLINNCFILVS--EDYT 866
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 797 PAVYGIRKIDVSMLENTTKTISIRPCAGPYCDCKRNSDVNDVCIYLDGGLLMAHNDVTT 856
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 867 -QTGDFFGEIGAVMNKLLTMGSKFKRTILYDYAMCRANKESSDGAHGLDPP----- 918
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 857 NQIGFFGEIDPISLMRLHVNISYAFNKSVDYQSVCEPAAKPGA-GHRSAYVPISVADI 915
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 919 ---NAFLSAYVMITVELVLVEY---NLCSMWHSDMTKAKKALQOTLEPQDTEPRADV 971
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 916 LQICMMAATAAAMWLSLLOQFLSLTFPRLLLEAVEMEDDFTASLSK-----QSCITEQTYF 970
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 972 SEPTIKETTCNIACEDCSKSFVIOQIPSSNLFMVVYDS--SCLCESVAPITMAPIRBYN 1023
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 971 FDNQCSKSSGVLDGCNSRIFHGKMLNTNLTINWESKTCPCDTRRLILQAEQTSBDGRN 1033
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 1030 ESLKCERLKAOKIRRPESCHGFHPEENARECGASLQAOT--VLLLPLLLMFS 1084
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1031 ---PCDMVKOPRYKRKGDPVCFDNNVLEDDYDGCAGVSGQLNPSLWYIIGIQLFLLMVS 1084
      : : : : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
US-09-452-007-4
: Sequence 4, Application US/09452007
: Patent No. 6140485
: GENERAL INFORMATION:
: APPLICANT: Franco, Rodrigo
: APPLICANT: Sun Chen, Ai Ru
: APPLICANT: Suey, David J.
: TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
: NUMBER OF INVENTION: CALCIUM CHANNEL SUBUNITS
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P. C.
: STREET: Two Millita Drive
: CITY: Lexington
: STATE: MA
: COUNTRY: USA
: ZIP: 02173-4799
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:

```

	APPLICATION NUMBER:	US/09/452,007
	FILING DATE:	
	CLASSIFICATION:	
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER:	US/08/713,118
	FILING DATE:	16-SEP-1996
	ATTORNEY/AGENT INFORMATION:	
	NAME:	Mata, Elizabeth W.
	REGISTRATION NUMBER:	38,236
	REFERENCE/DOCKET NUMBER:	ACC96-01
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE:	617-861-6240
	TELEX:	617-861-9540
	INFORMATION FOR SEQ ID NO:	4:
	SEQUENCE CHARACTERISTICS:	
	LENGTH:	1091 amino acids
	TYPE:	amino acid
	TOPOLOGY:	linear
	MOLECULE TYPE:	protein
	US-09-452-007-4	
Query Match	19.7%;	Score 1118.5; DB 4; Length 1091;
Best Local Similarity	28.4%;	Pred No.1:2e-98;
Matches 323;	Conservative 232;	Mismatches 461; Indels 121; Gaps 41
OY	14 ASALLAAL-LYAALGDVVRSEQDIPLSV-VKLMSAFGEIKTSIAKYSGSQLQKKYK	71
Dd	3 ACCLLALTTLTFLPSLLIGSSSEEPFSAVTIKSWDMQMEDLVTLAKTAGSVQLVDIYE	62
OY	72 EYEKVAIFEIDGLQVLVKLKAKNMEMFKKSEAVRLVEAAFEALKHKEFDADL---	OY 128
Dd	63 KYDDLYTEPPNAROLVELAARDIEKLISNRKALVSLALEAKYQAAMQWREDFASNEV	122
OY	129 EYFNANLINERPKDGNELFLGKEFI---LAPNDHFNNLPVNITSLDPVOPTMYNKNDPAI	185
Dd	123 VYYNKK--DDDEPEKNDSPEGSQRKPVIETEDANFER-OISTOHAANHPTDIESTTV	179
OY	186 VNGVYWSLANKVFVDFNPDRPDLIMQVPGSAGKGFROYPGIKWEPE--NGVIAFDCR	242
Dd	180 INELMWTSLADEVFKNRREDPSLLMQVGSAATGLARYYPASPWNDSRPKNIDLYDVR	239
OY	243 NRKWITQATSKDVYILVSDVSGSKGLRLTLAQIVSSILDTLGDDFFNIATVNEELH	302
Dd	240 RRPWYIOGAASPKDMLILDVSGVSGLTKLIRTSVSMLETSLDDDEVNAASFNSMAQ	299
OY	303 YVEPLNLGLVQADPRNKEPHREHLDKLFKAGIGMDIALNEAFNTLSDFNHTGGSIGS	362
Dd	300 DYS-CFO-HLVQANRNKKVULKDVAANNITAKGITDYKKCFSTREFOLLNVNRRAN-CN	355
OY	363 QAIMLTIDGADVDTYTIFAKYMPDPKRVARIFPYVLIGREAFAFDNLKMKMACAKNGEFTQIS	422
Dd	356 KIMFLTDDGGERAQEIFKNYN-KKKKVAVEFPFSVQHNYENRGPIOMMACENKGYYIELP	414
OY	423 TLADVOENVMEYLHLSRPKI--DOEHQVYTEAVIDSTLTDDOGPVLMTTVAAPVES-	479
Dd	415 SIGAIRINTOEVLVIGRMVLAGGAKAKOVMTNYLDAL---ELG--LVITGLTPVENI	469
OY	480 ---KQNFERSKG-TLLGVGTDPVPKELLKTIPKKGIGHGYAFAITNNGYILLTHRELH	535
Dd	470 TGOEFNKTNLKQQLLLGWGVDSVEDIKRLTRPFLTCPCNGYFIADIPGVALLRPNLO-	528
OY	536 LYEESKRRRKRRPYSSVDLSEVEMEDRDDV-LRNAVNRKTGK-FSMEVK----RTVDGK	588
Dd	529 ---PKPKSQGP-VLDELDALEENDIKVEINKKMIIDGESGEXTERTLVKSODEKRIDGK	584
OY	589 KRVLVMTDYTYTIDKTPFSIGVALSRHGKYFF-----RGNVTIEEGI-	633
Dd	585 NRT-----YTMTPVNGTDYSLALVLPY-YSPYYIKAKLEDITITQARSKKGMKQSETLK	637
OY	634 -HDLEHPVSLADEMSYCNTDLHPHRHLSOLEAIKLYLKGP--LIQCCKELIDVLEFD	691
Dd	638 PDNEEESQYTFIAPRDYCN-DLKSIDNNTTEFLINTNEFIDRKTTPNNPSCNADLIRNVLD	696


```

Db 580 NRT-----YWTVPVNGTDYSLALVLP-YSEYIYIKAKLEETITQARSKKGMKDETLK 632
QY 634 -HDEHPDVSLADEWSYCNTDLHPEHRHLSOLEAFTKLYKKEP-LLOCDKELIOEVLFD 691
Db 633 PDNFEESGYTIFAPRDYCN-DKISDNNTEFLNENEFIDRKTNNPNSCNADLINRVLLD 691
QY 692 A-VVSAPIEAYWTSIALNKSENSDKVEAFGLGTRTGLSRINLFVGAEOQLNODFLKAGD 750
Db 692 AGFTNELVQNYWS-----KQKNIGYKARFVVTGGITRVYP-----KEAGE 733
QY 751 KENTFNADHFLPMTARRAEQIIPGSFYISIPF-STGPVYKSNVYTASTSIQLLDERKSPV 808
Db 734 MNOENPETYEDSFYKRSLDN--DNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLK 791
QY 809 VAAVGIOKLEFFORRFPWTASROCASLDGKCSISCDDEFTVNCYLIDNNGFILVS--EDYT 866
Db 792 PAVVGIKIDVMSWIENTFKTISRDPACAGPVCDCKRNSDVMDCVILDDGGFLMANHDDYT 851
QY 867 -QTGDFEGEIGAVVNNKLLTNGSEFKRITLYDYQAMCRANKESSDGAHGLDPY----- 918
Db 852 NQIGHEFEIDPISLRHLVNIISVAFNKSVDYQSVCEPGAAPKGA-GHRSAYVPSVADI 910
QY 919 ---NAFLSAVMIMTELVLFLVER----NLCSWHSMDMTAKAQKQTLBPCDTEYPAFV 971
Db 911 LQIGMMATAAAMSILOQFLSLTFEPLLEAVEMEDDFTASLSK-----QSCITEQTOYF 965
QY 972 SERTIKETTGNIACEDCSKSFVIOIPSSNLFMVVYVDS--SCICESVAPITMAPIEIRYN 1029
Db 966 FDNDSKSFSSGLDCGNCGRIFRHEKLMNTNLIETIVESKGTCPCDTRLIIQAEOQSDGPN 1025
QY 1030 ESLKCERLKAKQIRRRPESCHGFHEENARECGAPSLQAQT--VLLLLPILLMLFS 1084
Db 1026 --PCDMVKQPRYRKGPVVCFDNNVLEDTDCGVSGLNPSLWYIIGIQFILLMLVS 1079

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Search completed: August 16, 2002, 22:19:12
 Job time: 7667 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 16, 2002, 20:21:55 ; Search time 11.02 Seconds
(without alignments)
1286.805 Million cell updates/sec

Title: US-09-787-657-5

Perfect score: 5667
Sequence: 1 MAGPSPRRASRGASALLAA.....SLQAQTVLLPLLMFSR 1085

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5524	97.5	1091	2	T30256
2	1148.5	20.3	1106	1	CHRB2
3	1122.5	19.8	1091	2	CHRB2
4	1114.5	19.7	1091	2	A44147
5	716.5	12.6	734	2	S44617
6	561	9.9	1148	2	T18770
7	203	3.6	1450	2	C86880
8	166.5	2.9	886	2	S54355
9	162.5	2.9	889	2	JC5576
10	160	2.8	570	2	AC2356
11	156.5	2.8	946	2	S54354
12	156.5	2.8	946	2	JC5575
13	154.5	2.7	946	1	IRH2
14	153	2.7	2166	2	G70163
15	152.5	2.7	914	2	JC5574
16	151.5	2.6	930	2	JX0368
17	146.5	2.6	1297	2	S39791
18	140	2.5	1021	2	T15900
19	139.5	2.5	1302	1	JC6009
20	139	2.5	5005	2	F82884
21	138.5	2.4	1127	2	T28317
22	138.5	2.4	1552	2	G86344
23	138.5	2.4	3724	2	T18427
24	138	2.4	436	2	E90261
25	138	2.4	1232	2	H91178
26	137.5	2.4	739	2	E97245
27	137.5	2.4	911	2	A39667
28	137	2.4	888	2	C90595
29	136.5	2.4	907	2	S54353

30	136	2.4	2401	2	T28676	rhodry protein -
31	135	2.4	1440	2	T33813	hypothetical prote
32	134	2.4	876	2	G89952	DNA polymerase I l
33	134	2.4	3135	2	A48584	transmission block
34	132.5	2.3	435	2	F96939	TPR repeats contai
35	132.5	2.3	885	2	S30350	inter-alpha-trypsi
36	132.5	2.3	906	1	JN0607	alpha-catenin 1 -
37	132.5	2.3	932	2	JC5953	inter-alpha-inhibi
38	132.5	2.3	1088	1	PIKPR	inner layer protei
39	132	2.3	758	2	C96749	hypothetical prote
40	131.5	2.3	649	2	B71826	type II DNA modifi
41	131.5	2.3	676	2	T47637	hypothetical prote
42	131	2.3	448	2	C82936	signal recognition
43	131	2.3	1377	2	D90538	hypothetical prote
44	130.5	2.3	811	2	AB1980	two-component hybr
45	130.5	2.3	3351	2	T13812	lipophorin - full

ALIGNMENTS

RESULT 1
T30256
calcium channel alpha-2-delta-C chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 20-Jun-2000
C:Accession: T30256
R:Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F.
J. Neurosci. 19, 648-691, 1999
A>Title: Molecular diversity of the calcium channel alpha2delta subunit.
A:Reference number: Z20794
A:Accession: T30256
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1091 <KLD>
A:Cross-references: EMBL:AV010949; PIDN:CAA09423.1
A:Experimental source: brain
C:Superfamily: calcium channel alpha-2 chain

Query Match	Best Local Similarity	Score	Pred. No.	Length
Matches 1064;	Conservative 2;	Mismatches 19;	Indels 6;	Gaps 1;
QY	1	MAGPSPRRASRGASALLAAALYALGDVRSQQIPLSVKIMASAFGEIKSI	60	
DB	1	MAGPSPRRASRGASALLAAALYALGDVRSQQIPLSVKIMASAFGEIKSI	60	
QY	61	SGSOLLQKKYKEYEKDAIEIDGLQVYKRLAKNMEEMFKKSAVRLVEAEALKH	120	
DB	61	SGSOLLQKKYKEYEKDAIEIDGLQVYKRLAKNMEEMFKKSAVRLVEAEALKH	120	
QY	121	EPFADLQYEFNVLINERKDGNEFLGKEFILAPDHNNPLVNSLDVQPTMYN	180	
DB	121	EPFADLQYEFNVLINERKDGNEFLGKEFILAPDHNNPLVNSLDVQPTMYN	180	
QY	181	KDAIVGVVSVSLNKVFVDFNDRDPSLIWQYFGSAKGFROYGKIWEDENGVIAPD	240	
DB	181	KDAIVGVVSVSLNKVFVDFNDRDPSLIWQYFGSAKGFROYGKIWEDENGVIAPD	240	
QY	241	CRRKRWITQATSPKDVVILVDSGSMKGLRTIAKTQVSSIDTLDGDDPFNTITANE	300	
DB	241	CRRKRWITQATSPKDVVILVDSGSMKGLRTIAKTQVSSIDTLDGDDPFNTITANE	300	
QY	301	LHVEPCNLGTIVQADRTNKEHREHDKLPAFGIGMIDALNEAFNLSDFNHTGSGI	360	
DB	301	LHVEPCNLGTIVQADRTNKEHREHDKLPAFGIGMIDALNEAFNLSDFNHTGSGI	360	
QY	361	CSOAIMLITDGAVDYDTIFAKYNMPPDKRVIFITYLIGREAPADNKKMACANKGFTQ	420	
DB	361	CSOAIMLITDGAVDYDTIFAKYNMPPDKRVIFITYLIGREAPADNKKMACANKGFTQ	420	
QY	421	ISTLADQENVMEYLAHLSRPKVIDGDEHDVVWVEAYIDST-----LTDDQGPVLMTTVA	474	

Db 421 ISLTADVQNMVEYLHLVLSRPKYLIDQEHQVMTAEAYIDSTLPQAKLADDOGLVMTTVA 480
Qy 475 MPVFSKQNETRSKGIILGVYGTDPVYKELTKTPKYLGIHGAFATNNGYILTHPELR 534
Db 481 MPVFSKQNETRSKGIILGVYGTDPVYKELTKTPKYLGIHGAFATNNGYILTHPELR 540
Qy 535 LLYEGRKKRRKPNYSSVDLSEVEWEDRDDVLRNAAVNRKTGKSMKVTVDKGRVLYV 594
Db 541 PLYEGRKKRRKPNYSSVDLSEVEWEDRDDVLRNAAVNRKTGKSMKVTVDKGRVLYV 600
Qy 595 TNDYVYTDIKGTGPFSLGVALSRGHGKFFRGVNTIEGHLHLEHPVSLADEMSTCNTDL 654
Db 601 TNDYVYTDIKGTGPFSLGVALSRGHGKFFRGVNTIEGHLHLEHPVSLADEMSTCNTDL 660
Qy 655 HEHRLHLSQLEAIKLYLKKEPPLQCDKELIOEVLFDVAVSAPIEAYMTSLANKSENSD 714
Db 661 HEHRLHLSQLEAIKLYLKKEPPLQCDKELIOEVLFDVAVSAPIEAYMTSLANKSENSD 720
Qy 715 KGEVAFGLGTGRLSLRINLFVGAEOULTNODFLKAGDKENIFNADHPLMYRRABEQIPGS 774
Db 721 KGEVAFGLGTGRLSLRINLFVGAEOULTNODFLKAGDKENIFNADHPLMYRRABEQIPGS 780
Qy 775 FYVSTPESFGPKNKSNVYTAISTIQLDKRSPVAAVGIOMKLEFFOKRFWTASQOCAS 834
Db 781 FYVSTPESFGPKNKSNVYTAISTIQLDKRSPVAAVGIOMKLEFFOKRFWTASQOCAS 840
Qy 835 LDGKCSISGDDPVCYLLDNNNGFIVSEDYTOTGDFEIGEGAVYNNKLLTNGSFRRITL 894
Db 841 LDGKCSISGDDPVCYLLDNNNGFIVSEDYTOTGDFEIGEGAVYNNKLLTNGSFRRITL 900
Qy 895 YDYQAMCRANKESSDGAHGLDLPYNAFLSAVKIMTELVLTFVEFNLCSMWSHSDMTAKAO 954
Db 901 YDYQAMCRANKESSDGAHGLDLPYNAFLSAVKIMTELVLTFVEFNLCSMWSHSDMTAKAO 960
Qy 955 KIKQPLEPDTEYPAFVSERTIKETTGNTACEDCSKSFYIOQIPSSNLFMYVYVDSCLCE 1014
Db 961 KIKQPLEPDTEYPAFVSERTIKETTGNTACEDCSKSFYIOQIPSSNLFMYVYVDSCLCE 1020
Qy 1015 SVAPITMAPIEIRYNESLKCERLKAQKIRRPESCHGFHPEENARECGAPSLAOATVLL 1074
Db 1021 SVAPITMAPIEIRYNESLKCERLKAQKIRRPESCHGFHPEENARECGAPSLAOATVLL 1080
Qy 1075 LPLPLMLFSR 1085
Db 1081 LPLPLVSSLEFSR 1091

RESULT 2
CHRA2
N:Alternate names: dihydropyridine-binding protein, 140K
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999
R:Ellis, S.B.; Williams, M.E.; Ways, N.R.; Brenner, R.; Sharp, A.H.; Leung, A.T.; Campbell, J. Biol. Chem. 265, 3287-3293, 1991
A:Title: Sequence and expression of mRNAs encoding the alpha(1) and alpha(2) subunits of A:Reference number: S10579; MUID:88336904
A:Accession: S10579
A:Molecule type: mRNA
A:Residues: 1-1106 <EHL>
A:Cross-references: EMBL:M21948; NID:9164762; PIDN:AAA81562.1; PID:g164763
A:Note: 57-Asn, 106-Lys, and deletion of 620-Ser were also found
R:Jay, S.D.; Sharp, A.H.; Kahl, S.D.; Vedyick, T.S.; Harpold, M.M.; Campbell, K.P.
J. Biol. Chem. 265, 3287-3293, 1991
A:Title: Structural characterization of the dihydropyridine-sensitive calcium channel al
A:Reference number: A39518; MUID:91131638
A:Accession: A39518
A:Molecule type: Protein
A:Residues: 961-973 <JAY>
A:Note: this sequence represents the amino end of a glycosylated peptide that appears at
e at the amino end and identical molecular weights (17k) following deglycosylation

R:Hamilton, S.L.; Hawkes, M.J.; Brush, K.; Cook, R.
Biochemistry 28, 7820-7828, 1989
A:Title: Subunit composition of the purified dihydropyridine binding protein from ske
A:Reference number: A33409; MUID:90122765
A:Accession: A33409
A:Status: preliminary
A:Molecule type: protein
A:Residues: 27-44, 'S', 46-47 <HAM>
C:Superfamily: calcium channel alpha-2 chain
C:Keywords: calcium; disulfide bond; glycoprotein; ion channel; membrane protein; pho
F:1-26/Domains: signal sequence #status predicted <SIC>
F:27-1106/Product: calcium channel alpha-2 chain #status predicted <MAY>
F:94,138,186,326,350,470,477,606,615,678,697,784,827,891,898,988,1001,1081/Binding s1

Query Match 20.3% Score 1148.5; DB 1; Length 1106;
Best Local Similarity 28.5%; Pred. No. 17e-63;
Matches 320; Conservative 234; Mismatches 440; Indels 129; Gaps 39;
Qy 33 SEQOILPLSY-VKIMASAFGEIKSIKAKYSGSOLQKKYKEYEKDVAIEIDGLVKKL 91
Db 25 SEEPFSAVATIKSWVDKMGEDLVTLAKTASGVHQLVDIEKYQDLTYVEPNARQVLELA 84
Qy 92 AKNMEEMFHKKSEAVRLVEAAEEAHLKHEPDADL--OYEFNAVLINERDKGNFLEL 148
Db 85 ARDIEKLINRSKALVRLALEAKYQAAHQWREDFASNEVYVNAK--DOLDPEKNDSP 142
Qy 149 GKKEFI--LAPNHFNNLPNINISLDQVPCNTNKPAPLVNCGVYSESLNKYFVDFD 206
Db 143 GSORIKPVFTIDANFRROVSYOHAHAHIPPDIEGSTYLNENMTSALDDVFKKREED 202
Qy 207 PSLIMQFSGSANGFPRQYGIKWEPE--NGVIAFDCNRKRYIOAATSPKDVYLVYD 263
Db 203 PSLIMQFSGSANGIAYYASPVWDNSRTPNKIDLDVARRRYIOGASPDMLILVYD 262
Qy 264 SSGMKGLRTTKQYVSSILDLGDDFPNITAYNEBELHYVEPCLNGTLVQADRKNKEFP 323
Db 263 SGSVSGLTGTLKLRISVSEMLETSLDDPFVNAVSFNSNADVS-CFO-HLYQANVRNKKYL 320
Qy 324 REHLDFAKGIGMDLIALNEAFNILDENHNGGSGISQALMLITGQVADYDTTFAY 383
Db 321 KQAVNNITAKKGLTDYKKGSPFAFEOILNTNVASAN--CNKILMLFTDGEENAOEIFAKY 378
Qy 384 NMPDRKVRITFYLLIGREAFAADNLKMKMACANKGFTQISTLADVQNMVEYLHLVSRPV 443
Db 379 N-KDKKVRVFTPSVQGHNDROPIDMACENKGYEYIETSAIRNTQGEYLDVGRPV 437
Qy 444 I--DOEHVYMTAEAYIDSTLTDGCVLMTFTVAMPVFS---KQNETSKG--ILGCVGT 496
Db 438 LAGDKAKOVQWNTNYLDAL--ELG--LVITGTLPLVFNTGOFENKTNLKNQILIGVGV 492
Qy 497 DVPVELLTKTIKYGKIGYAFATNNGYILTHPELR-----LYEGKKRRKPNYSS 550
Db 493 DVSLEIDIKRLTRFLCPGNYTFAIDPNGYVLLHPALQKPLGVGIPPTINLKKRRPNVON 552
Qy 551 -----VDLSEVEWEDRDDV--LRNAAVNRKTGK--FSMEVK---KTVDKGRVLYVT 595
Db 553 PKSGEPVTLDFDALELNDIKVEIRNKMIDGESGETFTFLVKSQDERIDGNT----- 608
Qy 596 NDYTTDIKGTGPFSLGVALSRGHGKFFRGVNTIEGHLHLEHPVSLADEM----- 647
Db 609 --YTTWTPVNGTSSIALVALPYPSFYIKAK--IEETITQAVSYETLKPDPNEESGTYFL 664
Qy 648 ---SYCNDLHPEHRLHLSQLEAIKLYLKKEP--LLQCKELIOEVLFDFA--VVSAPIEAYV 702
Db 665 APRDYC-SDLAKSDNNTEFLNLFNEFIKRTPNMPSCNTDLNRYLLDGLFTNELVQNTV 723
Qy 703 TSLANKSENSDKGEVAFGLGTGRLSLRINLFVGAEOULTNODFLKAGDKENIFNADHPEL 762
Db 724 S-----KQNKIKGVKARVYVTDGQITRYFP-----KAGEMQWGNPPEYEDS 765
Qy 765 WYRAABEQIPGSFYVSIPE--STGPNKSNVYTAISTIQLDKRSPVAAVGIOMKLEF 820

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Db 766 FYKRSIDN--DNYVFTAPYFNKSGPAGESGJMSKAVEIYIOGKLLPAVVGKIDVNS 823
QY 821 FQRKFTASROCASLDGKCSISODDETVNCYILDNGGFLTVS--EDYF-QTGPFEGIEG 877
Db 824 WIENFTKTSIRPCAGPYDCCKRNSVMDCVILLDDGGFLMANHDDYVNOIGRFGSEIDP 883
QY 878 AAMNKLITMGSEKRTILYDQAMCRANKESSDGAHGLDLPY-----NAFLSAVKV 927
Db 884 SLMRHLVNSVYAFNKSXYDQSCERGAAPKOGA-GHRSAYPSTADLQIGMWATAAAM 942
QY 928 INTELVLFIVER---NLCSMWSDMTAKAOKIKOTLEPCDREYPAFVSERTIKETGTNI 983
Db 943 SILQGFILSLTFEPRLLEADMEDDEDTASMSK-----QSCITEQGYFEDNDKSPFSGVL 997
QY 984 AEDCSKSVIOQIPSSNLFPMVYVDS--SCLESVAPITMAPLEIYIESLKCEBKAKQ 1041
Db 998 DGCNCSRIHFVBERKMTNLTIFIMWESKGTCPDPT---RLLIQAQNSIDGPPCDMWKOPR 1054
QY 1042 IRRPESCHGFHEENARECGA---PSTLQA---QTVLLLL 1076
Db 1055 YKKGPPVCHDNNVLEDTYDCGGVSGLNPMSLWITIGIOPVLLWL 1097

RESULT 3
JH0565
calcium channel alpha-2b chain precursor - human
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
C:Accession: JH0565
R:Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Vellicelebl, G.; Ellis, S.B.;
Neuron 8, 71-84, 1992
A:Title: Structure and functional expression of alpha1, alpha2, and beta subunits of a n
A:Reference number: JH0564; MUID:92110010
A:Molecule type: mRNA
A:Residues: 1-1091 <WID>
A:Cross-references: GB:M76559; NID:9179761; PIDN:AAA51903.1; PID:9179762
A:Experimental source: basal ganglia
A:Note: several conflicts are found between GenBank submission, authors' translation in
C:Comment: This protein is a subunit of the voltage dependent calcium channel.
C:Keywords: glycoprotein; phosphoprotein
F:1-24/Domains: signal sequence #status predicted <SIG>
F:25-1067/Product: calcium channel alpha-2b chain #status predicted <CAL>
F:32,268,326,539,635,1087/Binding site: phosphate (Thr) (covalent) (by protein kinase C)
F:91,142,250,623,817/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #sta
F:92,136,184,324,348,468,585,594,663,882,769,812,876,883,973,986/Binding site: carb
F:501/Binding site: phosphate (Thr) (covalent) #status predicted
F:833/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predic

Query Match 19.8%; Score 1122.5; DB 2; Length 1091;
Best Local Similarity 28.4%; Pred. No. 7,1e-62;
Matches 323; Conservative 233; Mismatches 460; Indels 121; Gaps 41;

QY 14 AASLLAAL-LVAALGDVVRSEQIPLSY-VKIMASAFGEIKSIAXKSGSGLLQKKY 71
Db 3 ACLAALTLTLTLOSLTIGSSSEPPSAVTIKSWDKMOEDLTAKTASGVQVLDIYE 62
QY 72 EYKDAVEIEIDGLQIVKKRLAKMEEMFHKSEAVRLVEAEAHKHEFDADL---QY 128
Db 63 KYQDLYTVEPNNAQVLELAARDIEKLNSRKALYSALAEKVOAAMQWRDEPFSNEY 122
QY 129 EYFNAVLIERKDKGNFELGKEFT--LAPNDHNNLFPVNISLSVOVPTNNKNDPAI 185
Db 123 VYVNAK--DDLPPEKNDSEPGSQRIKPVETIEDANFGR-GISYOHAAVHIPTDIYEGSTIY 179
QY 186 VNGVYSESLNVFYDNPEDRPSLIWQYGSAGKGFROYPGIWEDEE--NGVIAFDOR 242
Db 180 LMEIWNTSALDEYFKKNREDESSLMOVGSAFGARLYRPASWVUNSKRTPNKIDLYDVR 239
QY 243 NKNWYIQAAATSPRDVVIIVDVGSMKGLRLLTAKQTVSSILDTGDDFFNITAYNEELH 302
Db 1031 NKNWYIQAAATSPRDVVIIVDVGSMKGLRLLTAKQTVSSILDTGDDFFNITAYNEELH 302
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Db 240 RRPWYIQGAAPKMDLILVDGSGVSGLTLLKLTFTVSEMLETSLDDDFVVASFNSNAQ 299
QY 303 YVEPCLNGTIYQADRTRKKEFRELHDLKLPAGKIGMDIALNEAFNITSDPNHGGSGICS 362
Db 300 DVS-CFQ-HLYQANVRKKYKLDVANNITAKGITDYKKGSFAFEQILLNVNSPAN--CN 355
QY 363 QALMTLTDGAVDDYDITFEAFKNNPDRKVRJFTYLIGREAFADLKKMACANGFEFTQIS 422
Db 356 KIITMLTDDGEEERAOELFNKN--KDKKRVYFRSVGQHNTERGPIQMACEKNKGYIEIP 414
QY 423 TLADVOENVEVLYLHVSRPVY--DQEHVDVTEAYIDSTLTLDQGVLMITVAMPVS- 479
Db 415 SIGAIRINTQEDYDLGRPVVLGADKAKQYQMVNVYDAL---ELG--LVITGTLPEVNI 469
QY 480 ---KQNETRSKG--ILIGVSTDPVVKELLTIRKYLKIGIYAFATINNGYILTHPELRL 535
Db 470 TGOFEENTNLKNOLLIGVMQVDVSLDEIKRLTRFETLCPNGYFYAIDPNQVYLHPMIO- 528
QY 536 LYEGKKRRKPNYSVYDLSVEWEDRDDV--LRNAMVNRKTGK--FSMEVK---KTVDKG 588
Db 529 --PKNPKSQEP--VTLDFDLAELENDIKVEIRKMKIDGESGEKTFRLVKSODERTYDKG 584
QY 589 KRVLYMTNDYYTYDIDKGPSPSLGVALSRGHKGYFF-----RGNTYIEBGL- 633
Db 585 NRT-----YTWTPVNGTDSLALVLPY-YSFYIRAKLEETITQARKSKKKMKDSETLK 637
QY 634 -HDEHPDVSADWSTCNTDLHPEHRHLSOLEAIKYLKKEP-LIQCCKELIOEYLF 691
Db 638 PDNFEESGYFIAPRDYCN-DLKISDNTTEFLTNFEIRKTPPNNSCNADILNRYLDD 696
QY 692 A-VYSAPIEYVWYSLANKSENSDKGYEAFVFLGRSLINLNVGAEOQLNDQFLKAGD 750
Db 697 AGTTNELVQWYWS-----KQNKIKGVARPVTDGIGITVYP-----KEAGE 738
QY 751 KENIFNADHFLPWYRRAEOIPGSFYVSIPE--STGPNVSNVYASTSIQLDERKSPV 808
Db 739 NMQENPETYDSFYKRSLDN--DNYVFTAPYFNKSGPAGESGJMSKAVEIYIOGKLLK 796
QY 809 VAAVGIOMKLEFPQRKFWTASROCASLDGKCSISODDETVNCYILDNGGFLTVS--EDYT 866
Db 797 PAVVGIKIDVNSIENFTKTSIRPCAGPYDCCKRNSVDVDCVILLDDGGFLMANHDDYT 856
QY 867 -QTDGPFEGIEGAVMKNLITMGSEKRTILYDQAMCRANKESSDGAHGLDLPY----- 918
Db 857 NQIGRFGTEIDPSLMRLHVNISYAFNKSXYDQSCERGAAPKOGA-GHRSAYPSTADI 915
QY 919 ---NAFLSAVKWITELVLFIVER---NLCSMWSDMTAKAOKIKOTLEPCDTEYPAFV 971
Db 916 LQIGMWATAAAMSLIQFLSLTFEPRLLEAVEWEDDEDTASLSK-----QSCITEQGYF 970
QY 972 SERTIKETGNINACEDCSKFVYIQQIPSSNLFPMVYVDS--SCLESVAPITMAPLEIYRN 1029
Db 971 FDNDSKSFSGVLDCCGNCSTRIFHEKLMNTNLTIFIMWESKGTCPDPTRLLIQAQTS DGNP 1030
QY 1030 ESILKCEBKAKQIRRPESCHGFHEENARECGAPSLQOT--VULLLPLMLFS 1084
Db 1031 ---PCDWKOPRYRKGPVCFDNNVLEDTYDCGGVSGLNPMSLWITIGIOPVLLMWLS 1084

RESULT 4
A44147
calcium channel protein alpha-2 chain precursor - rat
N:Alternate names: dihydropyridine-sensitive L-type
N:Contains: calcium channel alpha-2 chain
C:Species: Rattus norvegicus (Norway rat)
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 20-Aug-1999
C:Accession: A44147
R:Kim, H.L.; Kim, H.; Lee, P.; King, R.G.; Chih, H.
Proc. Natl. Acad. Sci. U.S.A. 89, 3251-3255, 1992
A:Title: Rat brain expresses an alternatively spliced form of the dihydropyridine-sen
A:Reference number: A44147; MUID:92228762
A:Accession: A44147
A:Status: preliminary
```


QY 457 -----IDSTLDDGQVLMNTVAMPVFSKONETRSKGLLGVGTDPVPEKL 503
DB 478 SFAVANKMASRRKILQKSEARSRMFTVTYSEVLT--VNET-----FNGAAVNIPLTEV 550
QY 504 LKTIPIKYLIGHYAFATINNGYILTHPELRLYLEEGKKRRKPNSSVDLSEVEMEDRDD 563
DB 531 AKSHRPAHNGSGSYFFMMDQNGFVMTHPOLRPI-DFPTKYHKONYNMMDLELEFVGONON 589
QY 564 VLRNMAVNRKRTGFSME-----VKRTVDKG-----KRY 591
DB 590 V-RSSQSGQAVSDLVCESGANYAECDVDRKAVRKMIIDCDNSDVQOQLDVLATATELDTRY 648
QY 592 LMTNDYTYTDDIKGTFPSLGVALLSRG-----HGKYFRGVNTLIEGHLDEHPDVSL 643
DB 649 YQGTNTYTAECINHANFVGLAVAKGDDYRVYKKQKKYDF-GKVKMD-----NM 696
QY 644 ADE-WSYCNMTDLHPEHRHLSQLEAIK---LYLKGEPLL 678
DB 697 GDKRMR-----LHP-HMHVLEFEFKNFDMKIKYKVLPLV 730

RESULT 6
18770
probable calcium channel protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T18770; T25249
R:Stulston, J.
submitted to the EMBL Data Library, June 1995
A:Reference number: 219019
A:Accession: T18770
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1148 <W11>
A:Cross-References: EMBL:249907; PIDN:CAA90091.1; GSPDB:GN00020; CESP:T24F1.6
A:Experimental source: clone B0491
R:Chui, C.
submitted to the EMBL Data Library, June 1995
A:Reference number: 220004
A:Accession: T25249
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1148 <W12>
A:Cross-References: EMBL:249912; PIDN:CAA90141.1; GSPDB:GN00020; CESP:T24F1.6
A:Experimental source: clone T24F1
C:Genetics:
A:Gene: CESP:T24F1.6
A:Map position: 2
A:Intons: 91/2; 131/3; 170/3; 283/1; 322/2; 410/3; 487/1; 563/1; 602/3; 654/3; 683/3; 7

Query Match 9.9%; Score 561; DB 2; Length 1148;
Best Local Similarity 21.3%; Pred. No. 1e-26;
Matches 248; Conservative 213; Mismatches 441; Indels 260; Gaps 49;

DB 290 PPTITIDLPFRRPRPMVNAESVPKDIVFLDDSGSVKGTMLIKTMMYIILSTLSPND 349
QY 291 FENIIAVNEELHYVEPLCNGTLVQADRTNKHREHLDKLPK-----GICMLD 339
DB 350 YFGGVYFNHNFNPLISCANRTFMPATSNKKVFEEELGMELEKQDAHFAFPLKSLDYL 409
QY 340 IALNEAFNILDPNHNGGSGICSOAIMLITDGAVDYDTITFAKYNMP-----D 387
DB 410 GNLDNSQSLADYRSEGH-----KLIIFTDG--VD-----EMHQILDEEFQTRNS 454
QY 388 RKVRIFFYILGRFAAFADNLKMMACANKGFTFOISTLADVOENMEYLHSPRYVD-- 445
DB 455 ELIRIFGSMGYGTSLPLQOYMAKCSHGYSSELDSDMDKPSQRTIQNTLSVROGELK 514
QY 446 ----QEHVYMTAYIDSTLDDGQVLMNTVAMPVFSKONETRSKGLLGVGTDPVPEKL 501
DB 515 GTNAEKREPSMTQLYME---TQGTGPV--TLSPILTSBQRIWRDQKLAGVAIDISIK 569
QY 502 ELKTIPIKYLIGHYAFATINNGYILTHPELRLYLEEGK-KRRKPNSSVDLSE----- 555
DB 570 EFTKHLPTSEOMYGY--IVDNNGMILYHPOLIIPKTEVHCVRRSACYDAQVAKAGSG 627
QY 556 --VEMEDRDDVLRNMAVNRKTG-----KFSMEYKRTV--DKGRVLMT----- 595
DB 628 LRHYHGFSD-----RYRLVGLDLSIPTLMDLDEGDSFALRRLRITTKCYERAIK 682
QY 596 ---NDYTYTDDIKGTFPSLGVALLSRGHGKYFRGVNTLIEGHLDEHPDVSLAD----- 645
DB 683 DNSKEYSHIKDSPFLTVIV-----NNIQKTYVYDSDVQELGIDTKMLVTFE 731
QY 646 -----EMSYCNMTDLHPEHRHLSQLEAIKLYLKGEPLLQCKEL---IOEVLFDVAVS 695
DB 732 YPRRDVQOMRLDEYAADRERWSDISE-----KEICADDMRLPRAFTKLGSGWTQS 784
QY 696 AP---IEAYMTSLANKSEMSDKGVEY-AFLGRTGSLRINLFGABQL--TNODF---L 746
DB 785 WPKSDIE-HTTCLLAQVPEPAASVPHYVNSFVHRSKLTATAYPCSSHDMKAVKKPDEEI 843
QY 747 KAGDKENIFNADHPPLMYRRAEQIPGSFVYSIPFSTGPVKNKSNVYASTSIOLLDERKS 806
DB 844 KLIDNNDF-----VQFSM-----RSESLIYRTIADYDNNR- 874
QY 807 PVAAVGIGOMKLEFQKFFMTASRQCSLDGKCSISODDETVNGYLLIDNNGFIIVSDEY- 865
DB 875 --LAVGTQMKNEFFQDYFNFTRO--NPWKI--CRKO--ECSTIIRNGHYASSAHR 925
QY 866 --TQTDGFEEL-EGAVNKLITPMGSPKRTITLDYQAMCRANKESSDGAHGLDPYNAFL 922
DB 926 APRLAKFTDQLESLYKVLVINSTWTEV-----QSECKAKR-----VAPWSSAA 971
QY 923 SAVKWTMTLVLFVLENLCSWMSHSDM-----TAKAKIKQTLPEPCDE 966
DB 972 PGSSSLIRYVTSIFPLAKTSFMRNLLESALTLDVDAQPMTGMNCTFOKIK-PRERCFMK 1030
QY 967 YPAFVSERTIKETGTGNACEDCSKSFYIQIIPSNLFMVYVSDSCLESAVPTMAIEI 1026
DB 1031 FFHYRMTLNTKQLQLGMSGTSRYAKLIVPVPHTLSLIADRA--CSQYRPKRIFESEP 1088
QY 1027 RYNSLSKCRILKAKOIKRRPES 1048
DB 1089 KLE--KCDVYVHSH-ARRRPA 1107

RESULT 7
C86880
hypothetical protein yycC [imported] - Lactococcus lactis subsp. lactis (strain IL140
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: C86880
R:Polletin, A.; Wincker, P.; Mager, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Eh
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis

A:Reference number: AB6625; MUID:21235186; PMID:1133471
A:Accession: C86880
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1450 <SMO>
A:Cross-references: GB:AE005176; PID:q12725093; PIDN:AAK06141.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
C:Gene: yvcc

Query Match Similarity	3.6%	Score 203;	DB 2;	Length 1450;
Best Local Similarity	18.8%	Pred. No. 0.00036;		
Matches 211;	Conservative 167;	Mismatches 366;	Indels 380;	Gaps 55;

QY	30	VVRSEQOQIPLESVYVILMVSFGEIKSTIAKSGSQLLQKKYKXEYKQVALAEIIGDQLVK	89
Db	119	VLRRANNSISLNLLEIQADA-----KLIENDQGEVIDEDT-----LAK	154
QY	90	KLA-----KNEDEMRKSEAVRLVEAAEEHNLKHEEDA-----	124
Db	155	KESTIFSLYIPENKNAKSKDEKNKNTTEEVYLNNESSQOETYSOLKRLQALFSPYSNFGIK	214
QY	125	----DLOYEYENAVLINERDKGNFLELQKEFIAPARDHFNPNLVPVNLSDVOYPTMYN	180
Db	215	ASFNDLANQNTENISPEYRKQDETG-----ISPHSM-----IPTG----	248
QY	181	KDPAIVNGVYVSESLNKVEFVNDNEDRPSLIWQFSGA---KGFROYPGIKWDENGVI	237
Db	249	-NTTVNVHNGWNS-----FSSOMGWNVS--WN--GEATNLENSTIEYAGV-----NNPV	292
QY	238	AFDCR-----NRKWTYQOATSPKPDQVILVDSGSMGLRLTIAKOTVSS	281
Db	293	DFALRKAKKETETGCLDYVLINANGVONQPKRPDIYVLVDSGSMOGAKETAVRCQVSD	352
QY	282	ILDTLGDQD---DFEN--TIAVNEELHAYEPCLNCTLVOADRTNKEHREHLKFLA---K	333
Db	353	FLSTQMTAVADYVNVGIVGVSFGNVTGASGYTTPIDIKVSESHKSNOLAPQFS	412
QY	334	GIGMLDLALNFAFVILSDPNHTGGSGISCSQAIMITGA-----VPT--YDTI	379
Db	413	GGTTLQGLRKGTMTLMDQSDDNO-----KMLIMTDGVPTFSTKYKVASAKVDNVIYGOS	467
QY	380	FAK--YNNPDRKVRITFYVLIGREAAFADNLK---WMAK-----ANKGFTQISTLADVOE	429
Db	468	FAEERDEPQNTSKIOSPYVYKDIWGSGNIEIRDTWATLGEAEISKEISEIHTLQIQLG	527
QY	430	NVMEYLVLSRPKYIDOEHDVYVWLEAVIIDSTLDDQCPVLMTYAMVYFQKQWETSKEI	489
Db	528	NDGSY---LSQEEVKSRSTSLATTGCLQDQANSANDITDYLRKNO--ANVYLSRPN--TTTNGI	562
QY	490	LLGVGSTDVPVKEL-----LKTIPRYKLGINGVAF--ITYNNGYIITHPBELRL	535
Db	583	ILDELGAQEFKDTKFEITSVGESIDNLPRTKINEKGEIISMLNIGKNQEOVJHVOVRL	642
QY	536	LYE-----BEKKRRKRPYSSVD-----LSEYEW--EDDDVYL	565
Db	643	NTEFDKRTYVWQMNQETTLTPRGSNPNKVNFGVPASAKSSGINITLLEQWLANSENTP	702
QY	566	RNA--MVNRRKTGKFSMVCRTVDKGRKRVLWMTNDDYYTIDKGFPEISGLVALSGHGRKYFE	623
Db	703	ENVELLIGRSAQISSDMWTK-----VTLKEDDEMNSQLENP-----KYST	744
QY	624	RGAVTIEEGHLDHEHPVSLAD--EMSYCTD-----LHPRHRLSQL	664
Db	745	LG---EEFYIEIKDELIVLNSSEIYDWTTIGEDTTIANIEKFRLOLIKTSNHNNEPLSEV	800
QY	665	EAIKLYLKGEKPELLOCKRELQO---EVLFPDAV-----VSAP---IDAYVTSILA	706
Db	801	EPVLYKNSQGBE---IDKAVTNEKGELTLPKTLNLTNGEYQLHEIKSPGHSLEGCPMK--I	854
QY	707	LKNSKSDCKVEVAFLCTRTGL--SRINLVEGABOLTN---QDF-----LKAGDKENI	754

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Db      855 KTEFENGQPIKVD--GEQALADEHNKFMISLANTINDINVEEPNSVYIDKRAVDSEK 912
Oy      755 FNADHFPLMYRRAEQ-----TGSFVYSITPESTGP----- 785
Db      913 LDGAVFENLYQIESVDDELQQLKPLEITNNLPQ--LYALQESVSPNGYRDDVEHFHFRVK 970
Oy      786 VNKSNVYVASTSIQI--LDERKSPVVAAVQIQMKLEFPQRKFWTASRQASLDGKCSIC 843
Db      971 FNGSITVAIGSGCIDIPPLDENES-----GNGNLVYL 1000
Oy      844 DDEFTVNCYLIDNNGFILLVSEDYQIOT-----GDFSEIEGAVNKKILMG----- 887
Db      1001 NEE-----ENGDLHTLLIFYNQAVPPIQLEWDKIDDDFTSPLAG--VSFELTRIGRKST 1052
Oy      888 ---SFKRITLYD-----YQAMCRANKESDGHGHLIDPYN 919
Db      1053 DSDSVKRNISFDRLKTFNNFEGGFIITALKSNLDGGLYIYDINEN 1096

```

RESULT
S54355

5

Inter-alpha-trypsin inhibitor heavy chain 3 precursor - mouse

```
c;species: Mus musculus (mouse mouse),
C;Date: 15-Jul-1995 #sequence revisio
```

C:\Accession: 554355

C;Accession: S54355

R; Chan, P.; Risler, J.L.; Raguenez, G.; Salier, J.P.

Biochem. J. 306, 50

A;Title: The three heavy-chain precursors;

A; Reference number: S54353; MUID:95194320

A;Accession: 554355
A;Status: preliminary

A: Molecule type: mRNA

A;Residues: 1-886 <CHA>

A;CROSS-references: EMBL:X/0393; NID:g695635; PIDN:CAA49843.1; PID:g695636

Inter-alpha complex component 1

Query Match	2.9%	Score 166.5	DB 2	Length 886
Best Local Similarity	19.6%	Pred. No. 0.032		
Matches 160	Conservative 104	Mismatches 255	Indels 297	Gaps 37

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QY 71 KEYEKDAIIEIDOGUYYKLAKNMEEM-----FHKSEAVRULVAEABH 117
Db 110 KQYKAAVSQKKTAG--LYKASGRKEKFTVSYNVAAGSKVFFELYEELLKRNKGKYEY 167
QY 118 LK-----HEFDADLOYEYFNALVINEBKDKGNFLE--LGKEFLIAPNDHFNMLPV 165
Db 168 LKVQPKQLYRHFELDAHI-----FEPQJIMDAEASFITINDLSALTKSPSGKKGHYSF 223
QY 166 NISLSDVQ-VPT---NMRYKDPATVGVYUWSSLSKNKYDFNEFDRDPSLIMQYFGSANGFE 221
Db 224 KPSLDQOOSRCPSTDSLKNDFITVDV-RRSPGNVOJVN-----GYF 266
QY 222 RQYPGIKMEDEKGVYIAFDQRNRKRYQAQATSPKDVILIVDVSGSMKGLRTIAKOTYSS 281
Db 267 VHF----FAQQLRPV-----PKNIVYIDVSGSMSGRKIQOTREALLK 306
QY 282 ILDTLGDDEFFNIATVNEELHYVERPCLNGTLVQADPTKNEHREHLQKL----- 330
Db 307 ILDDVKEEDLDYLFILFSTDY---TTMKRHLQOATPANKLEAKTFVKNIHDSQMTNINDG 362
QY 331 FAKGIGLIDLALNEARNIISDFNHTQGSIGSQALMLITDGVADPTDYDILFAKYWMPDRKV 390
Db 363 LKGIETELMKARERD-----HYVERSTSIITML-TDGDANTGESRPEKIOENVRNA 412
QY 391 ---RIPTYLIGREAEAFADNLKW-----MACANKGFFTOISTLADVOENMEYLYLSRPK 442
Db 413 IGGKFLPYLNG-----FGNNLNVNFEETLALBENHGJARRIYEDSDPANIQLQGFYEVAVNP- 467
QY 443 VIDDEHDVYVTEAYIDSTLTDQGFVLMITTVAMPYFSQNETRSKGILLGAVGIDVYKE 502
Db 468 -----LTNVVEYVEYENA 480

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Oy 503 L+NI+PKYKIGIH+Y+AA+IL+IN+NOY+IL+TH+BL+RL+Y+EG+CK+RR+K+PN+SS+DL+SE+VE+ED+ 562
Db 481 I+LD+-----I+LR+NS+Y-----P+HP+-YD+GE+I-----498
Oy 563 D+LE+RNA+VN+RR+TK+GS+ME+VK+TV+DK+GR+VL+MD+NY+YT+DI+KG+TP+SL+VAL+SR+GH+KY+F 622
Db 499 -V+VAG+RL+VD+RM+DN+EK+DA+V-----G+HG+AL+- 522
Oy 623 FR+GN+VT+IE+GL+HL+DE+HS+LA+DE-----W+SY+CT+DL+HP+EH+RL+SL+EA+IK+YL 671
Db 523 --N+LT+TE+EV+-D+ME+ED+AL+AK+OG+Y+IF+GO+Y+ER+LA+MY+LT-----I+DL+EK+RR+NA 570
Oy 672 GK+EP+LL+O+Q+CE+LI+Q+EV+LF+DA+VV+SAP+LE+AV+W+SL+LN+KS+EN-----SD+K+CV+EA+VL+GT 724
Db 571 KG+DE-----K+EN+TA+BAL+DL+SL+KY+HP+VL+PT+SM+VT+K+ED+NE+DQ+SI+AD+NG+EA+FA+ET 624
Oy 725 RT+GS+RL+NL+EV+GA+B+Q+LT+NO+FL+KA+-G+DK+EN+IF+NA+HF+PL+MY+RA+EA+Q+IPG--SF+VS+IP 780
Db 625 TT+-----MS+FL+TL+QO+SS+OP+Y+Y+VD+B-----P+HF+II+-----Q+IP+KN+DS+IC+IP+ND 665
Oy 781 F+ST+GP+VN+K-----SN+VY+TA+ST+-SI+OL+DE+KK+SP+VNA+VG 813
Db 666 EK+PG+IV+AL+LI+OD+PY+TG+IV+TG+IL+IG+DR+SA+SS+RT+G 701

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RESULT 9

JC5576
inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Mar-1999
A:Accession: JC5576, PC4486
R:Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Shinohara, H.
J. Biochem. 122, 71-82, 1997
A>Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors
sin inhibitor heavy chain family.
A:Reference number: JC5574; MUID:97420688
A:Accession: JC5576
A:Molecule type: mRNA
A:Residues: 1-889 <NAK>
A:Cross-references: DDBJ:D89287
A:Experimental source: liver
A:Accession: PC4486
A:Molecule type: protein
A:Residues: 34-53;449-475;509-526 <NA2>
C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 were
detected. The three chains play important role for pancreatic cancer.
C:Superfamily: inter-alpha-trypsin inhibitor complex component II
E:236-239,664-865/Dissulfide bonds: #status predicted

Query Match	2.9%	Score 162.5	DB	Length 889
Best Local Similarity	22.2%	Pred No. 0.057		
Matches 107	Conservative 73	Mismatches 188	Intels 113	Gaps
Oy	49	FGGEIKSIAMAKYSSQLLQKKRYKEYEKDAVIAIEIDLQIVKIAKIMDEM-----	98	
Db	101	YPGNIKE-----KEYAQKOY-----DKAVSOGKTAGVYKASGRLEKFTVSYAVKAAS	148	
Oy	99	---PHKSEAVRRLVEAAEEAHLK-----HEFDALQIYEFAVLINRDKDGNFL	146	
Db	149	KVTELLIYEELKKHKKRYEMIAKYOKOLVIRFELDAHI-----FERDYSIMLDEASFI	204	
Oy	147	E---LGKEFIILAPNDHFNINLIVNISLSDOV-VFT---NMYNKDPALVNGVYSESILAKVF	199	
Db	205	TNNDIGSALTKFSFGKGGHVSFKRPSIDQORSCPTCDTSLNDDFTIVYDVN--RESPPGAVO	263	
Oy	200	VDNEFDPPSLIMQVFGSAGKFFROYGKIKMEPRBNVYFDFCRNRKMYTQAATSPKQDVI	259	
Db	264	VVN-----GYFVHF-----FAQGLPLVY-----PKNIYF	287	
Oy	260	LVYDGSMSKGLRLTIKAOYVSSILDTLGDDEFNIIATVNEELHYEPPJLNGTLVQADRTN	319	
Db	288	VIDISGMAKGIQDTGVALLKLTIDMKODDYDNLFIFSTGV---TWKDSLVQATPAN	343	

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QY 320 KEHFREHDKLEFAGSIGMLDIALNANFIIISDF--NHTGGSSICSOAMLTITGAVDTYD 3177
Db 344 LEAATFPRSRISDQMTINIGLLRGIRMLTDAREQHTVPERSTIIIML-TGSDAVTGE 4020
QY 378 TTFAYKNPDRKV--RIFTYLIGREAAFDNLKW-----MACANKGFQTISLADVOE 429
Db 403 SRPEKIOENVKRALEGRRPLNLG----FGNNLNYNPLEMTALENHQVARIYEDSDANL 458
QY 430 NYMEYLHLSRPKYVIOEDHVVMTAEVYIDSTLTDQGPVIMTTVAMPVFESKONETRSKG1 489
Db 459 QLOGFVEEVANPDLITNVEVE-----YENAILD-----LTKNSYPHFQDSGETAVAGR 506
QY 490 L 490
Db 507 L 507

```

hypothetical protein all14403 [imported] - Anabaena sp. (strain PCC 7120)
C:Species: Anabaena sp.
A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C:Accession: AC2356
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuriitz, T.; Sasamoto, S.; Watanabe, A.; Iriugu
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC2356
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-570 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA876102.1; PID:g17133539; GSEDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all14403

Query Match	Similarity	2.8%	Score 160;	DB 2;	Length 570;
Best Local Similarity	22.2%		Pred. No. 0.041;		
Matches 104;	Conservative	80;	Mismatches 190;	Indels 94;	Gaps 22
14	ASALLAALLVLAALGDVYSEEOIPLSVYKVLASAFGEI	----	KSIAKY	-----	60
141	ADLLANSPVYFMAQADVAGLQKVPDAKYALYAKTHNRIDDPSSPLGYVYHTAPTBSN	200			
QY	61	SSQSLQKKYKETE	----	KDAVLEETDGLQLYKTLAKNMEEMFHKKSEAVRILVEAEBA	116
Db	201	SLQTLVADYTSVSGRPELTIVAD	----	QTQPOIQIQISKTRRGVSTNSLAQIMV	256
QY	117	HLKHEFDADLOEYFNAVLINERDKGNFLGKEETILAPNHFNPLVNISLSDQVPT	176		
Db	257	--NGPFWASGVSYESVI	----	AANSLQOQOEYQIA	-----
QY	177	NMYNKDAPIVNGVYSESLINKVYVDNF	----	RDPSLIWQYFGSAGKGFROYPGI	-----
Db	294	TFTSNMRAIALVPNAPWVASADEKAGAEKFTIYWSPDA	----	OKFATDGLRGTGPVVALGAKF	351
QY	230	EFDENGVIA	-----	PDGRNKKWYIOATFSKPDVYIIVDVGSGMKGLTLTA	275
Db	352	SP-ERGVAQAQYDLSLRPRKPEVVDAMLKSMQ	----	EASKKSLVYVVYDSSGSMGKNLPRAY	409
QY	276	KOTVSSIIDTDDDFENIIAYNEELIHYEPCINGLTVOADRTNKEHREHLDKIFAKCI	335		
Db	410	QMTLQNYINELTKKEEDIALVDFDSEIR	----	VLVGTFOGRDGRGOVIFSGLRADGG	463
QY	336	GMULDIALNEAFNILSPFNTGGSGISQOAILITDS	-----	AVDTYDTIFAKYNN	PD 387
Db	464	TLIYDAAMQARMWLO	----	KRRREGAL	----
QY	388	RVRVETFLYIGREAAE	----	ADNLKMMACANKGFTQ	-----
				ISTL	ADVO
					428

[illegible]

Db	55	EINDLAIVMEAYÖRSSJETIIKIEEVOÖK	LNKNSNDPAEVEKKIAYHDSMLKOLDEITER	114
0y	102	KSEAVRRL-----	VEAAEB--AHLKHEPDADLOEYFAVAILNER	139
Db	115	VOENÖRÖLÖVQÖGKIVDLKSLTKGFNPÖ	IDBSVENLSNVEKED--KANKENLESIKIAS	173
0y	140	DK-DGNFLELGEKFTLAPNDHFNNL	PVNISLSDVÖPFTNMYNKPDAIVNGVWSESUNKY	198
Db	174	EKFPTNI-----KELVFE-----	KIDMLKEISLEYKDLANIEERKNDILVKG--NEKLDLE	222
0y	199	FVDNDRDPSLIMÖYFGSAKFFÖQYÖG	IKKEPDENY--IADCDRR-----KW	246
Db	223	FSDLEKEFEFNIGKYSKIEBSFNFEYN	-KYLLENISIELIMESVKKINKEDFTLNR	281
0y	247	XIOAFTSKDVAIIVD-----VSGSMKGLR	TLIKQIVSSITLPTIGDDEFNITAAVEEL	301
Db	282	NEELONAKRDLIVYDORSKEITKRLKED	-KLYLVADNEISSMSSFKDNYSRINSLESM	340
0y	302	HYVEPCNLGTLVQADRTNKEHREHRLD	KLFPAKGIGMDIALNEAFNILLSNHTGOGSIC	361
Db	341	-----RIEMKYEBOYDVDFPKFSQVEL	NLKNLYEDYEDKISQVDNNIR	385
0y	362	SOAILMLTD-----GAVDTYDTITFA	YNNPDKKVRFLTYTLIGREAFADNLKMAA	411
Db	386	ERVELSLDLNLSKMSVOSGAID-----	FK-RLEDSNGIYLEFKRK--FGADIEVS	436
0y	412	CANKCFPIQI-----STLADYÖEVM	MEYLHLSRPKVID--QEHVWVTEAYISTLTD-	464
Db	437	BSFKCDINOLKMOLESÖLLDVSINOE	KLIKLNLDNLISNFEELNGRRNNNY--SNLNDI	494
0y	465	---QGFVIMTTY--AMPVFSKONETR	RSKGILLGVGTDPVKELLTKTIPKYGLIHGYAF-	519
Db	495	NAKYATALPESIDSSSKRENOMESKYSF	-----TD-----KLTAGDESL--MYGEKFE	543
0y	520	-----AITNNGYILHPELRLLYE	BGKKRRKPNVSSVLSEVEMEDRDPVLR---NAAVN	571
Db	544	TLSEÖATNN-----YÖFÖDLNKL	LENIEIESFYNMEKÖTOETLKVDFNTSLIN	591
0y	572	RKTGFSMEVKKYVDGKRVLVMTNDY	-----YTDIKGNPS---LG	611
Db	592	IKD-----EIGKNIYEPDRYIDE	VANIIVTÖLESKLOYSKWÖGEMDSNLKNIE	640
0y	612	VALSRHGKYEFFRGNVTTIEBGLJH	LDHPDVSIADEWSYCYNTDLHPEHRHLSOLEATKLYL	671
Db	641	SOQINTNEPFLSLIÖIQDKDIE	LSESEVFNLSD-----HL--ÖKKALDMHG	685
0y	672	KGKEPILÖCDEKELIOEVLDAV	SAPLEAVYTSIALNKSSENSDKGVEAFUGTRTGLSRI	711
Db	686	SWKDELIALNKSLL-----DIKVS-	-ELLSSATL--KIESLEKDVN-----DRM	727
0y	732	NLFVABÖLUTÖDPLKAGDKRKNIN	ADHPFL--WYRRABÖLPGSRVVSIPSTGPGVYNK	788
Db	758	EYVL-----LKTGDISELVI	EKKELKDMSYSÖSDAILGIKEF-----INR	769
0y	789	SNVYVASTIÖLDERKSPVAAV	GIÖMKLEFFÖRKFEWTAASROCASIDGKCSISCD-	845
Db	770	ÖTEIILKDSYVMELE-	-----LAKKRDKNKNPIYSKIEGÖDVKIKDÖFKI	812
0y	846	---ETVNCYLIDNNGFT-----	LVSEDTYÖTGDPFGEIGEVANNKLLTMGSEFRIT	893
Db	813	ESEDILNPFKSÖLNEFISKLOIV	SNIKSDMÖKÖIDFDRISKDILINRRDJSINNEVDSK	872
0y	894	LYDYÖAMÖRANKESSDGHA	GLIDPYNMFSLAVKIMIMELVLFVEFNULGSMHSDMÖAKA	953
Db	873	LSDWÖS--KLEH-----ITVKI	ENLSSGK-----VDLPLD--SEVTTKI	909
0y	954	ÖKLÖKÖTLEPCÖTEY-----	PAFVSERTIKETTGNI-----ACEDCSKSFVIOQI	997
Db	910	KELKSIESLESYIEKIDEFR	NOGAIYSDDLÖDINNHFKRETERLEENLSKFFA--AVL	968
0y	998	PSSNLEFVAVDS-----	SCLCESAVITMADIETIRYNE	1030

Db 969 NNSSEFVKEVDSLQDKRRTDIASFQANIDITLDSLNVKFNND 1009

RESULT 15

JC5574

Inter-alpha-trypsin inhibitor heavy chain 1 - golden hamster

C:Species: Mesocricetus auratus (golden hamster)

C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000

C:Accession: JC5574; PC4484

R:Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinozawa, H.

J. Biochem. 122, 71-82, 1997

A:Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors

sin inhibitor heavy chain family.

A:Reference number: JC5574; MUID:97420688

A:Accession: JC5574

A:Molecule type: mRNA

A:Residues: 1-914 <NKA>

A:Cross-references: DDBJ:D89285; NID:g1694687; PID:BAAL3938.1; PID:g1694688

A:Experimental source: liver

A:Accession: PC4484

A:Molecule type: protein

A:Residues: 387-400:461-475 <NA2>

C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 were

that the complexes play important role for pancreatic cancer.

C:Superfamily: Inter-alpha-trypsin inhibitor complex component II

F:247-250,690-890/Disulfide bonds: #status predicted

Query Match 2.7%; Score 152.5; DB 2; Length 914;

Best Local Similarity 21.7%; Pred. No. 0.25; Indels 95; Gaps 20;

Matches 95; Conservative 73; Mismatches 174; Indels 95; Gaps 20;

```
OY 47 SAFGEIKSIKAKYSGSQLQKKYKYEKDVAEIIDLQLYKVLAKNMEK----- 98
Db 110 NTFIGDIDKAS-----ANKQYKRAISGENAG--LVRTSGRMEDQTTIITVGA 156
OY 99 -----FHKKSEAV--RLVE-----AAEEAHLKHEFDADLOVEYFNNAVLINERKDNFL 146
Db 157 QSKATFOLTYEVLKRRITQYKVKQVQVQHFEDV--DIEPQGISKLDAQASF 214
OY 147 --ELGKEFILAPNDHFNLPVNISLSDVQVPTNKNKDPALVNGVYSESLNKVVD-NF 203
Db 215 SKELAAQT--KESFSGKKGHLER---PTVSQOQPCPTCSTSWLNGDFKVTYDVNR 267
OY 204 DRDPSLIQWYGSAGKGFROYGKIMPEDENGVIAFDCCRNKKWYQAATSPKQVYILVDV 263
Db 268 DKLCDL-----VANNYFAHF-----FAPK-----LTNMSKNLVFVIDI 302
OY 264 SGSNKGRLRTIAKQTVSSILDTLGD--DDFNIIAYNEELHYEPCUNGTLVQADRTRK 320
Db 303 SGSMGQGV--KQTKKALLKILGDVKPGDSFDLVLFCSRVO---SWKSLVPATQANL 355
OY 321 ENFHREHDKLFKAKIGIMDLNFAFNILSDPNHTGGS---ICQATMLI-----TD 370
Db 356 QAADDFARFSLAATNLNGSLRGIEL---NKAQGSHPELSSPASILMLTLDGEPT 411
OY 371 GAVDTYDPIFAKYMWDKRVIRITFYILGREAFADNLKWMACANGFTQISTLADVOEN 430
Db 412 GETDRSQILKAVRNARIRFPLYNLNGFHDLD--NFLEVMSMENGMAQRTIYEDHDATQ 470
OY 431 VMEYLHLVSRPKVIDQ 447
Db 471 LQGFYNGVAVNPLTDVE 487
```

Search completed: August 16, 2002, 22:20:43
Job time: 7128 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 16, 2002, 22:19:16 ; Search time 61.26 Seconds
(without alignments)
685.777 Million cell updates/sec

Title: US-09-787-657-5

Perfect score: 5667

Sequence: 1 MAGPGSPRRASRGASALAA.....SLQAQIVLILPLLMFSR 1085

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1148.5	20.3	1106	C1C2_RABIT	P13806 oryctolagus
2	1122.5	19.8	1091	C1C2_HUMAN	P54289 homo sapien
3	1114.5	19.7	1091	C1C2_RAT	P54290 rattus norv
4	716.5	12.6	734	1 UN36_CAEEL	P34374 caenorhabd
5	167.5	3.0	935	1 ITH2_PIG	002668 sus scrofa
6	166.5	2.9	886	1 ITH3_MOUSE	061704 mus musculu
7	162.5	2.9	886	1 ITH3_MOUSE	P97280 mesocricetu
8	156.5	2.8	946	1 ITH2_MESAU	P97280 mesocricetu
9	156.5	2.8	946	1 ITH2_MOUSE	061703 mus musculu
10	154.5	2.7	946	1 ITH2_HUMAN	P19823 homo sapien
11	152.5	2.7	930	1 ITH4_MESAU	P97278 mesocricetu
12	151.5	2.7	930	1 ITH4_HUMAN	Q14624 h inter-alp
13	146.5	2.6	1296	1 ITH3_RAT	063416 rattus norv
14	146.5	2.6	1296	1 BXC_CLOBO	060393 clostridium
15	143.5	2.5	991	1 SC4A_RICAU	094616 rickettsia
16	137.5	2.4	911	1 ITH1_HUMAN	P19827 homo sapien
17	136.5	2.4	907	1 ITH1_MOUSE	061702 mus musculu
18	135.5	2.4	885	1 ITH3_HUMAN	006033 homo sapien
19	134	2.4	3135	1 S230_PLAFO	008372 plasmodium
20	132.5	2.3	906	1 CTR1_HUMAN	P35221 homo sapien
21	132.5	2.3	1088	1 RRO_POTPG	P17699 porcine rot
22	130	2.3	902	1 ITH1_PIG	029652 sus scrofa
23	129	2.3	1088	1 RRO_POTSI	P22678 simian 11 r
24	127.5	2.2	921	1 ITH4_PIG	P79263 sus scrofa
25	127.5	2.2	1584	1 U104_CAEEL	P23678 caenorhabd
26	127.5	2.2	1636	1 BRD3_YEAST	P25558 saccharomyc
27	127	2.2	1088	1 RRO_POTPG	P17699 porcine rota
28	127	2.2	1957	1 YDB6_SCHPO	010411 schizosacch
29	127	2.2	2366	1 TOXB_CLODI	P18177 clostridium
30	126.5	2.2	906	1 CTR1_MOUSE	P26331 mus musculu
31	126.5	2.2	1129	1 YB95_YEAST	P38144 saccharomyc
32	125.5	2.2	779	1 CN10_HUMAN	O9Y233 homo sapien
33	124	2.2	1088	1 RRO_POTBU	P21615 bovine rota

34	124	2.2	4092	1 DYHC_YEAST	P36022 saccharomyc
35	123.5	2.2	944	1 Y166_UREPA	O9P0X7 ureaplasma
36	123	2.2	810	1 CLPC_BACSU	P37571 bacillus su
37	122.5	2.2	1391	1 RPOB_MYCPN	P78013 mycoplasma
38	121.5	2.1	1033	1 SN11_YEAST	Q12038 saccharomyc
39	121.5	2.1	2105	1 POIR_ASQVP	P36309 apple stem
40	121	2.1	917	1 SYI_STPAU	P41972 staphylococ
41	120.5	2.1	5147	1 FAT_DROME	P33450 drosophila
42	119.5	2.1	1451	1 SPTE_YEAST	P23615 saccharomyc
43	119	2.1	1155	1 RPOB_BORBU	Q59191 borrelia bu
44	119	2.1	4568	1 DYHC_CAEEL	Q19020 caenorhabd
45	118.5	2.1	997	1 Y414_MYCPN	P75183 mycoplasma

ALIGNMENTS

```

RESULT 1
ID      C1C2_RABIT      STANDARD;      PRT; 1106 AA.
AC      P13806;
DT      01-APR-1990 (Rel. 14, Created)
DT      01-APR-1990 (Rel. 14, last sequence update)
DT      16-OCT-2001 (Rel. 40, last annotation update)
DE      Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta
DE      subunits precursor.
GN      CACNA2D1 OR CACNA2A OR CCH2A.
OS      Oryctolagus cuniculus (Rabbit).
OC      Mammalia; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Eukaryota; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX      NCBI_TaxID=9986;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=88336904; PubMed=2458626;
RA      Ellis S.B., Williams M.E., Ways N.R., Brenner R., Sharp A.H.,
RA      Leung A.T., Campbell K.P., McKenna E., Koch W.J., Hui A.,
RA      Schwartz A., Harpold M.M.;
RT      "Sequence and expression of mRNAs encoding the alpha 1 and alpha 2
RT      subunits of a DHP-sensitive calcium channel.";
RL      Science 241:1661-1664(1988).
RN      [2]
RP      SEQUENCE OF 961-973.
RX      MEDLINE=91131638; PubMed=1847144;
RA      Jay S.D., Sharp A.H., Kahl S.D., Vedvick T.S., Harpold M.M.,
RA      Campbell K.P.;
RT      "Structural characterization of the dihydropyridine-sensitive calcium
RT      channel alpha 2-subunit and the associated delta peptides.";
RL      J. Biol. Chem. 266:3287-3293(1991).
RN      [3]
RP      SEQUENCE OF 961-975; 992-1000 AND 1033-1050.
RX      MEDLINE=90368635; PubMed=2168391;
RA      de Jongh K.S., Warner C., Catterall W.A.;
RT      "Subunits of purified calcium channels. Alpha 2 and delta are encoded
RT      by the same gene.";
RL      J. Biol. Chem. 265:14738-14741(1990).
CC      -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN
CC      EXCITATION-CONTRACTION COUPLING.
CC      -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
CC      ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
CC      HETERODIMERS THAT ARE DISULFIDE-LINKED.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE
CC      SPLICING.
CC      -1- TISSUE SPECIFICITY: SKELETAL MUSCLE.
CC      -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM
CC      A PRECURSOR FORM.
CC      -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.
CC      -1- SIMILARITY: CONTAINS 1 VWF A DOMAIN.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way

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[illegible]

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Db      63 KYODLYVEPNNAQOLVEIARADIEKLLNSRKSALVSLALEAKYQAOAHQMFEDPASNVEV 122
QY      129 EYFNVAIILNERDKGNFLELQKEFI--LAPNDHFNNLIPVNISLDVQPTMYMKNDPAI 185
      123 VYNNK--DLDPEKNDSEFSQRIKRVFLEADNPFGR-QISYQHAVAHTPTDIEGSRIV 179
QY      186 VNGVYSESLKKEVFNDFDRDPSLIIMQYFGSAGFFRQYRGIKWEPDE--NGVIAFDOR 242
Db      180 LNELNWTSAIDLEVEKKNREEDPSILMOWFGSATGLARARYPASPMWNSRTPKIDLYDVR 239
QY      243 NRKWIIOAATSPKRVVILNDVSSGMGLKRTIAKOVYSSLDITDGDDEPFNIIANBELH 302
Db      240 RRPWYIOGAASPCKMLILNDVSGSVSLTKLRTISVSELEFLTDVDVNVASNSNAQ 299
QY      303 YVEPTLNTLVQADRTKNEHREHLOLQFKAGIGMDIALNEAFNLSDFNHTGGSGISCS 362
Db      300 DVS-CFO-HILOANVRKKRYLAKDAVNNTITAKGITTDYKKGFSAFEDLNVANSRAN--CN 355
QY      363 QAIMLITDGAVDYDTJFAKYNMDEKRVRIETYLIGREAAFDADNLKMACANKGFFTOIS 422
Db      356 KILMFTFGGEERAOEJFNKYN-KDKKVYFRFSVQGHVNERQIOWMACENKGYEYEP 414
QY      423 TLADQVENMVEYLVNLSRPVY--DOHDVNMFEAVIDSTLDDGDPVLMFTVAMPVVS- 479
Db      415 SIGAIRITQYLDVILSRPVLADKKKQYQWNVYLDL--ELG--LVITGLTPVENI 469
QY      480 ---KONETRSKG-ILGVGVDVYVKELLTIPKRYKLGIGHGAFTLNGGYTLTHPELRL 535
Db      470 TGQFENKTNLKNQILILGVMGVDSLEBTKLTFRFLTCRNGYTFALDPNGYLLHPNIO- 528
QY      536 LYEEGKKRRKKNYSSVDLSEVEMEDRDV-LRNAMVNRKTGK--ESMEVK---KTVDKG 588
Db      529 --PKPRSQEP--VTLDFLAELENDIKVEIRKMKIDGEGEXTPTLVKSDERYIDKG 584
QY      588 KRVLMTNDYIYTDIKTPPSGLAALSRGKGF-----RGVNTIEBL- 633
Db      585 NKT-----YMTVNTGTDVSLALVLEPT-YSFYIAKLEETITQARSKKGMKSEFLK 637
QY      634 -HDLHPDVSILADEMSVCNMDLPHREHRLSQLFAIKLYLKGKEP-ALOCDEKLEIOEVLF 691
Db      638 PDNFEESSYTLIARDYCN-DLKSIDNNTFELNPFNEFIDRKTNNPNSCNADLIRKVL 696
QY      692 A-VVSAPLEAVYTSIALNKSSENSDKVEVAFICTRGSLRINLFEVGAEOITNODFLKAGD 750
Db      697 AGFTNELQVNWYS-----KOKNIKGVKARFVVTGIGITRVYP-----KEAGE 738
QY      751 KENIFNADHFPLMKRRABEIQSGFVYSIFP--STGPVKNSNVYASTSIOULDERKSPV 808
Db      739 NMOENPETYEDSPFKRSIDN--DNVETAFYFKSPSGYAESGIMVSKVEYITOGKLK 796
QY      809 VAAVGIOMKLEFPQRKFMFASROCASLDKCSISCDENYVNCYLIDNNNGFIVS--EDYT 866
Db      797 PAVVGKIKDVMKLENTFKTISRPPCAGPYCDDCKRSSDVMDCYIILDGSEFLMAHHDYT 856
QY      867 -QTGDFEGEIGAVMNKILTMGSFKRTIYDYOAMCRANKESSDGAHGLDIPY----- 918
Db      857 NQIGRFPGEIDPSLMRLHVNISYVAFKSYDQYCEBPAARQGA-GHRSAYVPSVADI 915
QY      919 ---NAFLSAVYMWITELVYLVEF---NLCSMHSDMTAKAOKLQTLPECDTEYPAFV 971
Db      916 LQIGMWALAAAMWSILOOFLSLTFPRLLAEVEMEDDFTASLSK-----QSCITDQYGF 970
QY      972 SPRTIKETTGMIACEDSKSPVIOQIPSSNLPMVWYDS--SCLCESVAPITMAPIEIRYN 1029
Db      971 FDNDSKSPSGVLDCGNCSSRIFFHGKELMNTNLITIMESKGTCPDCTRLILOAEQISDQPN 1030
QY      1030 ESLKERLKAOKIRRPESCHGFHEPENARECGGASLSAQOT--VLLLPFLMLMS 1084
Db      1031 ---PCDMWKQGRYRKGPDVCGDNNVVLEDYTDGCGVGLNPSLWYITIGQFILLMWS 1084

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ID	CITC2 RAT	STANDARD:	PRT:	1091 AA.
DT	01-OCT-1996 (rel. 34, Created)			
DT	01-OCT-1996 (rel. 34, Last sequence update)			
DT	10-OCT-2001 (rel. 40, Last annotation update)			
DE	Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits precursor.			
GN	CACNA2D1 OR CACNA2A OR CCHL2A.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92228762; PubMed=1314383;			
RA	Kim H.L., Kim H., Lee P., King R.G., Chin H.;			
RT	"Rat brain expresses an alternatively spliced form of the			
RT	dihydropyridine-sensitive L-type calcium channel alpha 2 subunit."			
RT	Proc. Natl. Acad. Sci. U.S.A. 89:3251-3255(1992).			
CC	- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN			
CC	EXCITATION-CONTRACTION COUPLING.			
CC	- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:			
CC	ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS			
CC	HEXAMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).			
CC	- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE			
CC	SPlicing.			
CC	- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM			
CC	A PRECURSOR FORM (BY SIMILARITY).			
CC	- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.			
CC	- SIMILARITY: CONTAINS 1 VWFA DOMAIN.			
CC	-----			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL: M86621; AAA41088.1; "			
DR	InterPro: IPR004010; Cache.			
DR	InterPro: IPR002035; VWFA.			
DR	Pfam: PF02743; Cache; 1.			
DR	Pfam: PF00092; vwa; 1.			
DR	SMART: SM00327; VMA; 1.			
DR	PROSITE: PS50234; VWFA; 1.			
KM	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;			
KM	Calcium channel; Glycoprotein; Phosphorylation; Signal;			
KM	Alternative splicing.			
FT	SIGNAL	1	24	POTENTIAL.
FT	CHAIN	25	944	L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT
FT	CHAIN	945	1091	(BY SIMILARITY).
FT	CHAIN	945	1091	L-TYPE CALCIUM CHANNEL DELTA SUBUNIT (BY
FT	CHAIN	945	1091	SIMILARITY).
FT	TRANSMEM	445	468	POTENTIAL.
FT	TRANSMEM	506	930	POTENTIAL.
FT	TRANSMEM	1067	1086	POTENTIAL.
FT	DOMAIN	252	429	VWFA.
FT	CARBOHYD	92	92	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	136	136	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	184	184	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	323	323	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	347	347	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	474	474	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	584	584	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	593	593	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	663	663	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	769	769	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	812	812	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	876	876	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	883	883	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	973	973	N-LINKED (GLCNAC . . .) (POTENTIAL).

[illegible]

```
DB 855 YINQGRFGELGIDPMMRLVNIISLAFNKSYDQVCDPGAPKQK-GRHSAYVPSIT 913
      ||| | ||||| : || : : ||||| : ||| |
QY 919 ----NAPLSAVK-IMELVFL-----VEFNLCSMWHSMDTAKOKIKOTLEPCD 964
      : : : : : : : : : : : : : : : : : :
DB 914 DILQIGWMTAAWMSILOOLLLSTFEPRLLEAVEME-----BDDFTALSK-----QSCI 963
      : : : : : : : : : : : : : : : : : :
QY 965 TEYPAFVSERTIKETGTNACEDCSKSFYIOQIPSSNLFMYVDS--KCLCESVAPITMA 1022
      ||| | : : : : : : : : : : : : : : : :
DB 964 TEQOTYFFNFNDKTSFSGLDGCGNCSRIFFHEKLTMTNLFVINESKGTGPTCDT--RLIM 1020
      : : : : : : : : : : : : : : : : : :
QY 1023 PIEIRYNESLKCERLKAOKIRRRPESCHGFHEBNARECGA----PSIDA-----QTVLL 1074
      : : : : : : : : : : : : : : : : : :
DB 1021 QAEQSDGPDPCDMVKQPRYRKGPVCFNNVLEDTDCGVSGLNPSILMSIFGLPIILL 1080
      : : : : : : : : : : : : : : : : : :
QY 1075 LL 1076
      |
DB 1081 WL 1082

RESULT 4
UN36_CAEEL STANDARD; PRT; 734 AA.
AC P34374;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Protein unc-36.
GN UNC-36 OR UNC-72 OR C50C3.11.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Nilsson R., Alnsough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kersey J., Kilsten J., Lalister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sprat J.,
RA Woldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
CC -1- SIMILARITY: TO CALCIUM CHANNEL ALPHA-2B SUBUNIT.
CC -1- SIMILARITY: CONTAINS 1 VFMA DOMAIN.
CC -----
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CC -----
DB EMBL: L14433; AAA27969.1; -
DB PIR: S44617; S44617.
DB WormPep: C50C3.11; CE00117.
DB InterPro: IPR004010; Cache.
DB InterPro: IPR002035; VFMA.
DB Pfam: PF00743; Cache: 1.
DB Pfam: PF00092; vma: 1.
DB SMART: SM00327; VMA; 1.
DB PROSITE: PS5034; VFMA; 1.
KW Ionic channel; Ion transport; Voltage-gated channel; Calcium channel;
KW Glycoprotein.
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FT DOMAIN 250 435 VFMA.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 476 476 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 514 514 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 734 AA; 85034 MW; CCFB78C8DE4B71F CRC64;

Query Match 12.6%; Score 716.5; DB 1; Length 734;
Best local Similarity 27.9%; Pred. No. 1,1e-37;
Matches 212; Conservative 133; Mismatches 276; Indels 139; Gaps 26;

QY 23 LYALGDVVRSEQIPLSVYKLMASAFGEIKSLAAKSSQLQKKYKEKEDVAIEI 82
      | | | | : : : : : : : : : : : : : : : :
DB 6 LVLVATVYSTSSFNKESIKCAKYLSEMKTFKTSKISHETLIK--QNYEKLYEEQF 62
      : : : : : : : : : : : : : : : : : :
QY 83 DGLQIVKKLAKNMDEMHKSEAVRRLVEAAEHLKHEEDA-DLOYEYFNAVILINERD 141
      | | | | : : : : : : : : : : : : : : : :
DB 63 DPAEELKSKHRIEDYLKRSQFAKYAKISLEARSVANDSTVNDPOSKPIREMSAKQGN 122
      : : : : : : : : : : : : : : : : : :
QY 142 DGNFL-----ELG-----KEFLAPNDHFNNLPVNISLSDVOVPMNMKDPATVNGV 189
      | | | | : : : : : : : : : : : : : : : :
DB 123 DGTITESNLGKRLKRYNETKSFNLQNAFYLPTISSVSAHIIPTPLDRNEDLLRKI 182
      : : : : : : : : : : : : : : : : : :
QY 190 YMSSELNKVFVDNFDRLPSLIWQYFGSAKGFPOYQGIK--WEPDENGVIAPDCRNKMY 247
      | | : : : : : : : : : : : : : : : : : :
DB 183 DMSD-IDAVYRTNREETKDLAFLQFCSEAGYMRYPAAFWFMDQENHDLDFCQRTNEM 241
      : : : : : : : : : : : : : : : : : :
QY 248 IQAATSPKDVIIIVDVSNGSKGLRLTAKQTVSSIIDLDDDEFENIAANEELHYEPC 307
      | : : : : : : : : : : : : : : : : : :
DB 242 INSATSKNVLLIMDSGSMIGORYEVAKQTELELTLSHNDFFNMTSKMTFLDGC 301
      : : : : : : : : : : : : : : : : : :
QY 308 LNCT--LVQADPTNKEHFREHLDLKFAKIGMDIALNEAFNILDSPNHTG---QGSICS 362
      | | | | : : : : : : : : : : : : : : : :
DB 302 -NCTNGLTQTMNKKRLRKMDTYQSEGAKEYEKKALPLAFSVLLDINNCGGNRRGACE 360
      : : : : : : : : : : : : : : : : : :
QY 363 QAIMLTGCGAVDTYDTFAKYNMPDRKVRIFLYILIGEAAPADNLKMAKANKGFPTQIS 422
      | | | | : : : : : : : : : : : : : : : :
DB 361 NVIMLTIDGAPNAYKRIFFDMYN-ADKKRVFETPLVGSEADIDFEVRMACNNRGYVHVA 419
      : : : : : : : : : : : : : : : : : :
QY 423 TLADVENVEVYLVSRPVIDOHDVY--WPEAY----- 456
      | | | | : : : : : : : : : : : : : : : :
DB 420 NMADVDEKIHITRRMSR--VGRHRYKESGLSMWTVYERLRLPPELPAEVPITNQ 477
      : : : : : : : : : : : : : : : : : :
QY 457 -----IDSLTDDQGPVLTMTVAMPVFSKQNETRSKGLLGAVGTDVPYKEL 503
      : : : : : : : : : : : : : : : : : :
DB 478 SFAYMNMKMASRRKRIQLQKSEARSMEFTVTSVPYI--VNET-----FMGAVAANIPLTEV 530
      : : : : : : : : : : : : : : : : : :
QY 504 LKTIPIYKKGIGHGAFAITNGYILTHPELRLLYEBSKKRRKPNYSVDLSEVWEDRD 563
      : : : : : : : : : : : : : : : : : :
DB 531 AQKSHPANIGSKSYFFMLDNGCFVMTHPQLRPI-DEPTKYHKQNYNMDDLELEVGON 589
      : : : : : : : : : : : : : : : : : :
QY 564 VLKNAVNRKRTGFMSF-----VKTKYDKG-----KRY 591
      | | : : : : : : : : : : : : : : : :
DB 590 V-RSSQKSVQVSDLVCSGANVACVDDLRKAAVKRIIDCONSDVQDQDLVATELLDRY 648
      : : : : : : : : : : : : : : : : : :
QY 592 LVMTNDYVYVYDIKGFPSLGLVALSRG-----HGKYFFRGVNTYIEGLHLEHPDVL 643
      | | | | : : : : : : : : : : : : : : : :
DB 649 YPQNTNYYACINHANFVGLAVAKGDYRVVKKOKKYD-GRKKMD-----NM 696
      : : : : : : : : : : : : : : : : : :
QY 644 ADE-WSTCNTDLPHRRHLSQLEAIK---LYLKGKPELL 678
      | : | | | | : : : : : : : : : : : :
DB 697 GDKRWR-----LHP-HWVHFLFEFFKFMFKYIKVKLPLV 730
      : : : : : : : : : : : : : : : : : :

RESULT 5
ID ITH2_PIG STANDARD; PRT; 935 AA.
AC 002668;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
```


KM Serine protease inhibitor; Repeat; Signal; Multigene family;
 FT Glycoprotein. 1 18 POTENTIAL.
 FT SIGNAL 19 30 BY SIMILARITY.
 FT PROPER 31 646 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
 FT CHAIN 31 646 H3.
 FT PROPER 647 886 BY SIMILARITY.
 FT DOMAIN 279 439 WMFA.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT BINDING 646 646 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
 FT (BY SIMILARITY).
 SQ SEQUENCE 886 AA; 98977 MW; 15955308C7E5030A CRC64;
 Query Match 2.9%; Score 166.5; DB 1; Length 886;
 Best Local Similarity 19.6%; Pred. No. 0.0089;
 Matches 160; Conservative 104; Mismatches 255; Indels 297; Gaps 37;
 QY 71 KEKDYAIEIDGLQYKLAKNMEEM-----FKKSAVRLVEAAEAH 117
 DB 110 KQEKAVSQKTAG--LVASGRKLEKFTVSVVAAGSKVTFELLYELLKRNKGYEM 167
 QY 118 LK-----HEPDALQYEFNAVLINERDKGNFLE--LGKEFLAPNDFHNLV 165
 DB 168 LKQPKQVLRHFIDAH-----PEPGISMLDAASFITDGLSALTRFSKGKHYSF 223
 QY 166 NISLSVQ-VPT--NMYNKPAIVNGVWSESLNKFVDFNDRPSLIMQYFGSAKGF 221
 DB 224 KPSLDQQRSPCTDLSLNDGFTIVDVN-RESPGNVQIVN-----GYF 266
 QY 222 ROVPGIKMPEDENGVIAFCORNRKWTQAATSPKDVILVDVSGSKGLTLAKQVSS 281
 DB 267 VHF-----FAPOGLPVV-----PKNIVFVDVSGSGSKGRKIQGTREALLK 306
 QY 282 ILDTLGGDDFFNIAYNEELHYEPCLNGTLVQADRTNKEHREHLKL----- 330
 DB 307 ILDDVAKEDYLNLFSTVD---TTWKDHLVQATPANLKEATFYVANHIDQSTNTINDG 362
 QY 331 FAKGIMDLALNEAFNIISDFNHGOGSICSOAIMLTDGAVDYFTTFKATNMPDRKV 390
 DB 363 LKKGIMLNKARDD-----HTVERSTSLIIML-TGDANTGHSREKIQEENRNA 412
 QY 391 ---RIFTYLIIGRAAFADNLK-----MACANGFPTQISTLADYQINWMEYLHVS 442
 DB 413 IGGKFLYING---FGNNLNINPLETTLAENGLARITIEDSDANIQLQGFEEVAVNP- 467
 QY 443 VIDQEHVVTVEAYIDSTILDQGPVLMVTVAMPVFSKQNETRSKGIILGVGTGVPE 502
 DB 468 -----LNTNVEYEYENA 480
 QY 503 LKTIKPKYKLGIGHVAFATNNGYILTHPELRLLEYEGKKRRPNY;SVDLSEVEMED 562
 DB 481 ILD-----LTRNSY-----PHF--YDGSSEI----- 498
 QY 563 DVLNANMVRNKGKESMEYKKTVDKGRVLYMINDYITDIKGTPE;LGVALSNGHGYF 622
 DB 499 -VAGRLVVRNMDNFKRADYK-----GHCAL- 522
 QY 623 FRGNVTIEGLDLEHDPVSLADE-----WSYCTDLPHRHLSOLEAIRLYL 671
 DB 523 --NDLFTTEV-DMEEMDAIKEGYIFGDIYERLWAYLT-----IEQLLEKRNA 570
 QY 672 KGEKPLQCDKELLIOELVPAVVASPIEAVYSLAKNSN-----SDKGEVAVFLGT 724
 DB 571 KGE-----KENITAEALDLSLKYHVPPLTSMVVTKKPEDNDQETSIANAGEEAPET 624
 QY 725 RUGLSRLNLFVGAEOQLNDELKA-GDKENIFNADHPEPLMYRAAEIPG--SFVYSIP 780
 DB 625 TT-----MSFLTQQSSQSFYYVVDG-----PHFIT-----DIPGKNDISICPNID 665
 QY 781 FSTGPVNR--SNVVTAST-SIQLLDERKSPVAVAG 813

DB 666 EKPGTVLRLLQDPVTVGTGIVTQIIGDKRNSNSRTG 701
 RESULT 7
 ID ITI3_MESAU STANDARD; PRT; 886 AA.
 AC P97280;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy
 DE chain H3) (C33).
 GN ITI3.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=97420688; PubMed=9276673;
 RA Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
 RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain
 RT precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:
 RT implications for the evolution of the inter-alpha-trypsin inhibitor
 RT heavy chain family.";
 RL J. Biochem. 122:71-82(1997).
 RN [2]
 RP SEQUENCE OF 31-50; 446-472 AND 504-523, AND SUBUNITS.
 RC TISSUE=plasma;
 RX MEDLINE=97018241; PubMed=8864857;
 RA Yamamoto T., Yamamoto K., Sinohara H.;
 RT "Inter-alpha-trypsin inhibitor and its related proteins in Syrian
 RT hamster urine and plasma.";
 RL J. Biochem. 120:145-152(1996).
 CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
 CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
 CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
 CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
 CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
 CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN.
 CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-1) IS COMPOSED OF H1, H2
 CC AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
 CC BIKUNIN. AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
 CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
 CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ITI3 FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 WMFA DOMAIN.
 CC -----
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 CC -----
 CC EMBL; D89287; BAA13940.1; -;
 DR InterPro: IPR002035; WMFA.
 DR Pfam: PF00092; vwa; 1.
 DR SMART: SM00327; vwa; 1.
 DR PROSITE: PS50234; WMFA; 1.
 KM Serine protease inhibitor; Repeat; Signal; Multigene family;
 FT Glycoprotein. 1 18
 FT SIGNAL 19 30 POTENTIAL.
 FT PROPER 31 646 BY SIMILARITY.
 FT CHAIN 31 646 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
 FT PROPER 647 886 BY SIMILARITY.

Db 424 PTYGLKLSKIQKNVKQIOD-NISLFSIGIGFDVY-DFLKRLSNENRGIQRITYGNRD 481
QY 427 VOENMEYLHVLSRPKYIDQEHVDVWTEAYIDSTLTD 463
Db 482 TSSQKKFEYNQVSTPLLRNVQFN-----YPOASVTD 512

RESULT 9
ID ITH2_MOUSE STANDARD: PRT: 946 AA.
AC Q61703;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2).
GN ITH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6N; TISSUE=Liver;
RX MEDLINE=95194326; PubMed=7534067;
RA Chan P., Ristler J.-L., Raquenez G., Sallier J.-P.;
RT "The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse: new members of the multicopper oxidase protein group with differential transcription in liver and brain."
RL Biochem. J. 306:505-512(1995).
CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).
CC -1- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
CC -1- PM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ITI FAMILY.
CC -1- SIMILARITY: CONTAINS 1 VMFA DOMAIN.
CC -----
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CC -----
DR EMBL: X70392; CAA49842.1; -
DR MGI: 96619; Itln2.
DR InterPro: IPR002035; VMFA.
DR Pfam: PF00092; vwa; 1.
DR SMART: SMO0327; VMA; 1.
DR PROSITE: PS50234; VMFA; 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 18
FT PROPEP 19 54
FT CHAIN 55 702
FT PROPER 703 946
FT DOMAIN 308 468
FT CARBOHD 118 468
FT CARBOHD 263 463
FT CARBOHD 445 445

BY SIMILARITY.
INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2.
BY SIMILARITY.
VMFA.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

FT BINDING 702 702 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
FT SEQUENCE 946 AA; 105927 MW; 40DB6716433ED9DC CRC64;
SQ

Query Match
Best Local Similarity 24.5%; Pred. No. 0.042;
Matches 53; Conservative 56; Mismatches 90; Indels 17; Gaps 6;

QY 254 PKDVILVDVSGSKGLRLTAQVSSILDTLGDDEFNIAYNEELAYEPLCLGTLV 313
Db 308 PKNLFIVDVSGSMGKQVEAKMTLDDLTDFDQFSVDNF--HNVFTWRN-DLV 363
QY 314 QADRTKEHREHLDLFAKIGIMDLALNEARNIISDFNHTQGSICS-QALMLITDGA 372
Db 364 SATKTIADAKRYIEKIOPSQGTINELALRAFLINEASNMGLNPDVSLIILVSDG 423
QY 373 VDTYDTIFAKYNMPDRK-----VRIFTYLGRAFAFADNKKMACANKGFFTOISTLADV 427
Db 424 PTYGLKLSKIQKNVKQIODNISLFSIGIGFDVY-DFLKRLSNENRGIQRITYGNDR 482
QY 428 QENMEYLHVLSRPKYIDQEHVDVWTEAYIDSTLTD 463
Db 483 TSSQKKFEYNQVSTPLLRNVQFN-----YPOASVTD 512

RESULT 10
ID ITH2_HUMAN STANDARD: PRT: 946 AA.
AC P19823; Q15484; Q14659;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (inter-alpha-trypsin inhibitor complex component II)
DE (Serum-derived hyaluronan-associated protein) (SHAP).
GN ITH2 OR IGHERP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=88152237; PubMed=2450046;
RA Gebhard W., Schreitmüller T., Hochstrasser K., Wächter E.;
RT "Complementary DNA and derived amino acid sequence of the precursor of one of the three protein components of the inter-alpha-trypsin inhibitor complex."
RT FEBS Lett. 229:63-67(1988).
RN [2]
RP SEQUENCE OF 384-865 FROM N.A.
RX MEDLINE=88068576; PubMed=2446322;
RA Sallier J.-P., Diarra-Mehrpour M., Sesboue R., Bourguignon J., Benarous R., Ohkubo I., Kurachi S., Kurachi K., Martin J.-P.;
RT "Isolation and characterization of cDNAs encoding the heavy chain of human inter-alpha-trypsin inhibitor (I alpha TI): unambiguous evidence for multipolypeptide chain structure of I alpha TI."
RT Proc. Natl. Acad. Sci. U.S.A. 84:8272-8276(1987).
RN [3]
RP SEQUENCE OF 384-766 FROM N.A.
RX MEDLINE=89076497; PubMed=2462430;
RA Sallier J.-P., Diarra-Mehrpour M., Sesboue R., Bourguignon J., Martin J.-P.;
RT "Human inter-alpha-trypsin inhibitor. Isolation and characterization of heavy (H) chain cDNA clones coding for a 383 amino-acid sequence of the H chain."
RT Biol. Chem. Hoppe-Seyler 369:15-16(1988).
RN [4]
RP PARTIAL SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88024442; PubMed=3663330;
RA Schreitmüller T., Hochstrasser K., Resinger P.W.M., Wächter E., Gebhard W.;

RT "cDNA cloning of human inter-alpha-trypsin inhibitor discloses three
RL different proteins." ;
RN Biol. Chem. Hoppe-Seyler 368:963-970(1987).
[5]
RP SEQUENCE OF 55-74; 116-137; 224-246; 295-307 AND 365-385.
RX MEDLINE=99380192; PubMed=2476436.
RN Enghild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;
RA "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin
RT inhibitor, pre-alpha-trypsin inhibitor, from human plasma.
RT Polypeptide chain stoichiometry and assembly by glycan." ;
RL Biol. Chem. 264:15975-15981(1989).
[6]
RN SEQUENCE OF 55-64.
RP TISSUE-Plasma;
RX MEDLINE=93039735; PubMed=1384548;
RN Melki N., Baldyck M., Mees P., Capon C., Mizon C., Han K.K.,
RA Tartat A., Fournet B., Mizon J.;
RT "The heavy chains of human plasma inter-alpha-trypsin inhibitor: their
RT isolation, their identification by electrophoresis and partial
RT sequencing. Differential reactivity with concanavalin A." ;
RL Biol. Chem. Hoppe-Seyler 373:1009-1018(1992).
[7]
RN SEQUENCE OF 55-64 AND 681-702, CROSS-LINK STRUCTURE, AND
RP CARBOHYDRATE-LINKAGE SITES T-691.
RX MEDLINE=93232026; PubMed=7682553;
RN Enghild J.J., Salvesen G., Thøgersen I.B., Valnikova Z.,
RA Pizzo S.V., Helga S.A.;
RT "Presence of the protein-glycosaminoglycan-protein covalent cross-link
RT in the inter-alpha-inhibitor-related proteinase inhibitor heavy chain
RT 2/dikunin." ;
RL J. Biol. Chem. 268:8711-8716(1993).
[8]
RN SEQUENCE OF 67-101, AND HYALURONAN BINDING.
RP TISSUE-Serum;
RX MEDLINE=94075371; PubMed=7504674;
RN Huang L., Yoneda M., Kimeta K.;
RA "A serum-derived hyaluronan-associated protein (SHAP) is the heavy
RT chain of the inter-alpha-trypsin inhibitor." ;
RL J. Biol. Chem. 268:26725-26730(1993).
[9]
RN SEQUENCE OF 699-702, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE.
RP TISSUE-Plasma;
RX MEDLINE=94229087; PubMed=7513643;
RN Morelle W., Capon C., Baldyck M., Sautiere P., Kouach M.,
RA Michalski C., Fournet B., Mizon J.;
RT "Chondroitin sulphate covalently cross-links the three polypeptide
RT chains of inter-alpha-trypsin inhibitor." ;
RL Eur. J. Biochem. 221:881-886(1994).
[10]
RN CARBOHYDRATE-LINKAGE SITES, AND MASS SPECTROMETRY.
RP MEDLINE=98434966; PubMed=9677377;
RX Flahaut C., Capon C., Baldyck M., Ricart G., Sautiere P., Mizon J.;
RA "Glycosylation pattern of human inter-alpha-inhibitor heavy chains." ;
RL Biochem. J. 333:749-756(1998).
[11]
RN CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=98087700; PubMed=945062;
RA Olsen E.H.N., Rahbek-Nielsen H., Thøgersen I.B., Roepstorff P.,
RA Enghild J.J.;
RT "Posttranslational modifications of human inter-alpha-inhibitor:
RT identification of glycans and disulfide bridges in heavy chains 1 and
RT 2." ;
RL Biochemistry 37:408-416(1998).
[12]
RN FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SPERM OR AS A
RP BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.
CC -1- SUBUNIT: 1-ALPHA-1 PLASMA PRESEASE INHIBITORS ARE ASSEMBLED FROM
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN.
CC BIKUNIN, INTER-ALPHA-INHIBITOR (1-ALPHA-1) IS COMPOSED OF H1, H2
CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (1-ALPHA-L1) OF H2 AND
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-1) OF H3 AND BIKUNIN.
CC

[illegible]

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OY 425 ADVQENVMEXLHVLSPKVIDOEHDVWTEAYIDSTLTD 463
DB 480 QDTSSQKFKFYNOVSTPLLRNVOFN-----YPHISVTD 512

RESULT 11
ID ITIH1_MESAU STANDARD: PRT: 914 AA.
AC P97278:
DE 15-JUL-1998 (Rel. 36, Created)
DE 15-JUL-1998 (Rel. 36, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inter-alpha-trypsin inhibitor heavy chain H1 precursor (ITI heavy
chain H1) (HCl).
GN ITIH1.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=97420688; PubMed=9276673;
RA Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain
RT precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:
RT implications for the evolution of the inter-alpha-trypsin inhibitor
RT heavy chain family."
RT J. Biochem. 122:71-82(1997).
RN [2]
RP SEQUENCE OF 387-401 AND 461-475, AND SUBUNITS.
RC TISSUE=Plasma;
RX MEDLINE=97018241; PubMed=8864857;
RA Yamamoto T., Yamamoto K., Sinohara H.;
RT "Inter-alpha-trypsin inhibitor and its related proteins in Syrian
RT hamster urine and plasma."
RT J. Biochem. 120:145-152(1996).
RN [3]
RP FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
CC SIMILARITY).
CC -1- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
CC AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN (BY
CC SIMILARITY).
CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARATE (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
CC -1- SIMILARITY: CONTAINS 1 WMPA DOMAIN.
CC -----
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CC or send an email to license@isb-sdb.ch).
CC -----
CC EMBL, D89285; BAA13938.1; .
CC InterPro: IPR002035; WMPA.
CC Pfam: PF00092; wma: 1.
CC SMART: SM00327; WMA: 1.
CC PROSITE: PS50334; WMPA: 1.
CC Serine protease inhibitor; Repeat; Signal; Multigene family;
CC Glycoprotein.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 675 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN

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FT PROPER 676 914 H1.
FT DOMAIN 293 453 POTENTIAL.
FT CARBOHYD 288 288 WMPA.
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 591 591 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT BINDING 675 675 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CHONDROITIN 4-SULFATE, CROSS-LINK SITE
FT (BY SIMILARITY).
SQ SEQUENCE 914 AA; 101785 MW; B693FE956FE89E3 CRC64;

Query Match 2.7%; Score 152.5; DB 1; Length 914;
Best Local Similarity 21.7%; Pred. No 0.071;
Matches 95; Conservative 73; Mismatches 174; Indels 95; Gaps 20;

OY 47 SAREGEIKSIANKYSGSQLQKKYKEXEKDVAIEIDGLVKKAKMEEM----- 98
DB 110 NTFIGDIKDKAS-----AMKQYRKAIISGNAG---LVRTSGRMDEFTIHIVGA 156
OY 99 -----FKKSEAV--RRIVE-----AAEBAHKHEFPADLOEYFNVLINERKDGNFL 146
DB 157 QSKATFQLTVEEVLKRLTYDIYIKVKPKQLVGHFEIDV--DIEPQGISKLDAQSFL 214
OY 147 --ELGKEFIILPNDHFNNLPVNISLSDVOYPTNNYKNDPAIVNGVYSESUNKVFD--NF 203
DB 215 SKELAQTI---KESFGKKGHVLF---PTVSQOQOQPCPTCTSMUNDKFTTYDYNR 267
OY 204 DRDPSLIWOYFGSAGGFROYPGIKWEPDENGVIAPDCRRKKWYIOAATSPKDVILLVDV 263
DB 268 DKLCDDL-----VANNYFAHF-----FAPKN-----LTNNSKNLVFVIDI 302
OY 264 SGSKGKGLRLTAKQVSIIDTGLD---DFFNIATANEELHYEPLCNGLVQADPTNK 320
DB 303 SSGSNEGQKV---KQTKALLKILGLDVKRGSFIDLGLGSRVQ---SMKSLVPATQANL 355
OY 321 EHFREHIDKLEFANGIGMIDLALNEAFNLISDFNHTGGSS---ICSQALML-----TD 370
DB 356 QAAQDFYRRSLAGATMLNGLLRGIEL-----KKAQSHNELSPSPSIIMLTLDGEPT 411
OY 371 GAVDTYDTIFAKYMWPPRKRIEFTYLLIGREAFADNLKMAACANKGFTQISTLADVOEN 430
DB 412 GEFTRSQILKNVRNRAIGRPFLYMLGFGHLDL--NFLFVSMENSGMAQRTEBDHDAQ 470
OY 431 VMEYLHVLSPKVIDOE 447
DB 471 LOGFYNOVANPLDLTVE 487

RESULT 12
ID ITIH4_HUMAN STANDARD: PRT: 930 AA.
AC Q14624; Q15135; Q99054;
DE 15-JUL-1998 (Rel. 36, Created)
DE 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inter-alpha-trypsin inhibitor heavy chain H4 precursor (ITI heavy
chain H4) (inter-alpha-trypsin inhibitor family heavy chain-related
protein) (IHRP) (Plasma kallikrein sensitive glycoprotein 120) (PK-
120) (GP120) [contains: GP57].
GN ITIH4 OR IHRP OR ITIH1 OR PK120.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=95293915; PubMed=7775381;
RA Saguchi K.-I., Tobe T., Hashimoto K., Sano Y., Nakano Y., Miura N.-H.,
RA Tomita M.;
RT "Cloning and characterization of cDNA for inter-alpha-trypsin
RT inhibitor family heavy chain-related protein (IHRP), a novel human
RT plasma glycoprotein."

```

RN	J.	Biochem.	117:14-18(1995).
RP	[2]		
RC	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.		
RX	TISSUE-LIVER:		
RA	MEDLINE=95104473; PubMed=7805892;		
RA	Nishimura H., Kakizaki I., Muta T., Sasaki N., Pu P.X., Yamashita T.,		
RA	Nagasawa S.;		
RT	"cdna and deduced amino acid sequence of human PK-120, a plasma		
RT	kallikrein-sensitive glycoprotein.";		
RL	EELS Lett. 357:207-211(1995).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=96389995; PubMed=8797089;		
RA	Saguchi K., Tobe T., Hashimoto K., Nagasaki Y., Oda E., Nakano Y.,		
RA	Mura N.H., Tomita M.;		
RT	"Isolation and characterization of the human inter-alpha-trypsin		
RT	inhibitor family heavy chain-related protein (IHRP) gene (ITHIL1).";		
RL	J. Biochem. 119:898-905(1996).		
RN	[4]		
RP	PARTIAL SEQUENCE, AND CHARACTERIZATION.		
RC	TISSUE-Plasma:		
RX	MEDLINE=95332266; PubMed=7541790;		
RA	Choi-Mura N.-H., Sano Y., Oda E., Nakano Y., Tobe T., Yanagishta T.,		
RA	Tanigaya M., Katagiri T., Tomita M.;		
RT	"Purification and characterization of a novel glycoprotein which has		
RT	significant homology to heavy chains of inter-alpha-trypsin inhibitor		
RT	family from human plasma.";		
RL	J. Biochem. 117:400-407(1995).		
CC	-1- FUNCTION: MAY BE INVOLVED IN ACUTE PHASE REACTIONS.		
CC	-1- TISSUE SPECIFICITY: LIVER-SPECIFIC.		
CC	-1- INDUCTION: LEVELS INCREASE SIGNIFICANTLY IN THE SERA OF PATIENTS		
CC	AFTER DIFFERENT SURGICAL TRAUMA.		
CC	-1- PTM: CLEAVED BY PLASMA KALLIKREIN TO YIELD 100- AND 35-KDA		
CC	FRAGMENTS, AND THE RESULTING 100-KDA FRAGMENT IS FURTHER CONVERTED		
CC	TO A 70-KDA FRAGMENT.		
CC	-1- PTM: APPEARS TO BE BOTH N- AND O-GLYCOSYLATED.		
CC	-1- SIMILARITY: BELONGS TO THE TTH FAMILY.		
CC	-1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.		
CC	-----		
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch). -----		
DR	EMBL; D38595; BAA07602.1; -;		
DR	EMBL; D38535; BAA07536.1; -;		
DR	EMBL; U43163; AAD05198.1; -;		
DR	EMBL; U42015; AAD05198.1; JOINED.		
DR	EMBL; U42016; AAD05198.1; JOINED.		
DR	EMBL; U43155; AAD05198.1; JOINED.		
DR	EMBL; U43156; AAD05198.1; JOINED.		
DR	EMBL; U43157; AAD05198.1; JOINED.		
DR	EMBL; U43158; AAD05198.1; JOINED.		
DR	EMBL; U43159; AAD05198.1; JOINED.		
DR	EMBL; U43160; AAD05198.1; JOINED.		
DR	EMBL; U43161; AAD05198.1; JOINED.		
DR	EMBL; U43162; AAD05198.1; JOINED.		
DR	MIM; 600564; -;		
DR	InterPro: IPRO02035; VWFA.		
DR	Pfam: PF00092; vwa; 1.		
DR	SMART: SM00327; vwa; 1.		
DR	PROSITE: PS0234; VWFA; 1.		
KW	Serine protease inhibitor; Repeat; signal; Multigene family;		
KW	Glycoprotein.		
FT	SIGNAL	1	28
FT	CHAIN	29	661
FT	PROPEP	662	688
FT	CHAIN	689	930
CT			
		70 KDA INTER-ALPHA-TRYP SIN INHIBITOR HEAVY CHAIN H4. POTENTIALLY ACTIVE PEPTIDE. 35 KDA INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4.	

FT	DOMAIN	272	432	WMFA	N-LINKED (GLCNAC. . .) (POTENTIAL)	.
FT	CAROHAD	81	81		N-LINKED (GLCNAC. . .) (POTENTIAL)	.
FT	CAROHAD	207	207		N-LINKED (GLCNAC. . .) (POTENTIAL)	.
FT	CAROHAD	517	517		N-LINKED (GLCNAC. . .) (POTENTIAL)	.
FT	CAROHAD	577	577		N-LINKED (GLCNAC. . .) (POTENTIAL)	.
FT	CAROHAD	696	696		O-LINKED (GLCNAC) (PROBABLE)	.
FT	CAROHAD	701	701		O-LINKED (GLCNAC) (PROBABLE)	.
FT	CAROHAD	702	702		O-LINKED (GLCNAC) (PROBABLE)	.
FT	DISLPTD	747	925		PROBABLE	.
FT	CONFLICT	85	85		N -> I (IN REF. 2).	
FT	CONFLICT	85	85		N -> K (IN REF. 3).	
FT	CONFLICT	114	114		S -> N (IN REF. 1).	
FT	CONFLICT	207	207		N -> F (IN REF. 4).	
FT	CONFLICT	221	221		O -> E (IN REF. 4).	
FT	CONFLICT	307	307		R -> V (IN REF. 4).	
FT	CONFLICT	322	322		W -> Y (IN REF. 4).	
FT	CONFLICT	816	817		ET -> OR (IN REF. 4).	
SO	SEQUENCE	930 AA;	103358 MW;		DE1929065F4EB6A0 CRC64;	
Query Match						2.7%: Score 151.5; DB 1; Length 930;
Best Local Similarity						19.7%: Pred. No. 0.085; Mismatches 365; Indels 287; Gaps 45;
Matches 191; Conservative 125; Mismatches 365; Indels 287; Gaps 45;						
Qy	67	OKKYEYEKDVIAEIIDGLQVKKLAKNMEEFHKKSEAVRVLVEAEHKLHFEADL	126			
Db	97	EKAEMAOQSAAVAKGKSGLVKATGRNMEQ-----QVSVAVPRAKLTFE-----L	144			
Qy	127	OYEYRNAVLINRDKDGNLELG-KEPLI--APNDHNNLPVNISLDVQVNTMYKNDP	183			
Db	145	VE-----ELKKR-----LGVLELLKKRPQOLVXHLQMDIHIFEPQ-----	182			
Qy	184	ATVNGVWSESNKFEVDNFDPSLIQOFGSAGKGFROYGIMWP-----DE	233			
Db	183	-----GISPLET-ESTFMNQVLDAITLQ--NKTANHFRKLTLSQOQKSPQOETVLDG	235			
Qy	234	NGVIAFDCC-----NRKWTQ-----AATSPKDVVLVDVSGSMKGLRTIAKQ	277			
Db	236	MLIIRYDWDRAISGSGIOIENGVEFHYAPABEGLTTPMKPNVVFIDKSSMSGRKIQOTRE	295			
Qy	278	TWSSLDLTLDGDDFNIIIAVNEELHYVEPCUNGLTVQDRTKKEHFRHLQKLFKAGTGM	337			
Db	296	ALIKLIDLSPDQDNLIVFSTEATQWPR---SLVPSAENVKARKSPAGTIALGCTN	351			
Qy	338	LDIALNEAFNILDEN---HTGGSGICSOALMLITDGAVDYDT-----IFAK	382			
Db	352	INDAMLMVQLDSSNQEBRLPEGSV--SLTLLDGDPTVGETNPRSTIONNVREAVSGR	409			
Qy	383	YNNPDKRRIFFYLLIGREAFADNLKMAACANKGFTTQISTLADVQEVNMEYLHLSRP-	441			
Db	410	YS-----LFLGFGFDVSA-FLEKIALDGLGARRIHEDSDALQDLYOEAVNPL	461			
Qy	442	-----KVIDOEHVNV--TEAVIDSTLTDDGCVLMTTVAAMPFSSKONETR	485			
Db	462	LTAVFEXYPSNAVEEVQNNFRLLFKGSEMVYAGKL-QDRGVDVLTVNVSCKLPTQNTTF	520			
Qy	486	SKGILLGVGVDPVKELKTITPKI-----KGIH-----	515			
Db	521	O-----TESSVAQOEAEFQSPKFIHNFMRLLVAYLLTQILEQTVSASDADQALRN	573			
Qy	516	-----GYAFITNGVILTHPELRLLEYEGKKRRKPNYSVDLSEVEMEDRDQVLRNA	568			
Db	574	QALNLSLAVSEYVTLTSMVYTKPDDQ---EQSQAVERP-----MEGESRN--RNV	618			
Qy	569	MVNRKTKFSMEVKKTYDVGKRVLVMTNDYYTIDIKTQPSLGVALSGHGKYEFRGNVT	628			
Db	619	HSGSTFFKYVLOGAK-----IPKPEASFSPPRCNNRQAGAASRMM-----FRPGLV	665			
Qy	629	IEEGHLDHEHDPVSLADEMSYCNDLHNEHNLQSLER-ILYLLKGRPPLQOQKEL-IQ	686			
Db	666	SSRQGLGPGRPDV--PDHAAY-----HP-FRRLALPISADPATSNDPVAISRVMNMKTE	717			
Qy	687	EVLFPAAVVASPIEAVWTSLALNKSENSDKGVEVAFGLGRTLSLRINLPGAEQ--LTNQ	743			

Db 718 ETTMTTQTPAPIQAPSALPL-----PGOSVERLCVDPRHROGPVNLSDPEQGVETQ 772
Qy 744 -DELKAGDK--ENINADHFL-WYRAAEQIPGSEFVSIPESTGPVNSVNTASTSIQ 799
Db 773 YEREKAGSEWIEVTEKFN---PLVWVHASPEHV-----VTRNRSS 810
Qy 800 LLDKSPVAVAVGQIMKLEFFQKFWTASRCASLDKCSISCODEYVNCILIDNNGFI 859
Db 811 AVKMETLEFSVMPGLKMTM-----DKTGIL 835
Qy 860 LVSE-DYTGQDFGEIEGAVNKKL-----TMGSFKRTLLDYQAMCRANKE 906
Db 836 LLSDDPKYITIGLLFWDGCEGLRLLRDTDRSSHVGGLGQFYQEVLMGSPA-----A 889
Qy 907 SSDGAHGL 914
Db 890 SDDGRRTL 897
RESULT 13
ID ITI3_RAT STANDARD: PRT; 887 AA.
AC Q63416;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy chain H3).
GN ITI3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Rattus.
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RA Blom A., Fries E.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).
CC -1- SUBUNIT: 1-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN. AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ITI3 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 WMA DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send_an_email_to_license@sib-sib.ch).
CC -----
CC EMBL; X83231; CA58233.1; .
CC InterPro; IPR002035; WMA.
CC Pfam; PF00092; wma; 1.
CC SMART; SMO0327; WMA; 1.
CC PROSITE; PS02034; WMA; 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family; Glycoprotein.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 33 BY SIMILARITY.

FT CHAIN 34 647 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
FT PROPEP 648 887 H3. SIMILARITY.
FT DOMAIN 282 442 WMA.
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 580 580 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT BINDING 647 647 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
FT SEQUENCE 887 AA; 99097 MW; 3B9F0F96D514096 CRC64;
SQ

Query Match 2.6%; Score 148.5; DB 1; Length 887;
Best Local Similarity 17.4%; Pred No. 0.12;
Matches 142; Conservative 127; Mismatches 244; Indels 303; Gaps 37;

Qy 60 YSGSOLLQKK--KYEKEDVAIEIDGLQVKKIARME-----MFKKSE 104
Db 101 YPGS-VKEKEVAQKQYKAVSQKTAG--LVKASGRKLEKFTVSVNVAAGSKVIFELTVE 157
Qy 105 AVRRLVEAEALHK-----HEFDADLOEYNAVILNRRDKGNFL--LGER 152
Db 158 ELKRRKRGYEMYLKQPKQVLRHFEIDAH---FEQGISMLDADASEITNDLGSAL 213
Qy 153 ILAPNDHFNNLPVNISLSVQ--VPT---NMYNKDPALVNGVYSESLINKFVDFNDRPS 208
Db 214 TRFSQKKGHVSKRPSLDQORSCPTCTDILNDFTIYIVN--RESPGNQIYN----- 266
Qy 209 LHWQYGSAGKGFPRQYPGIKWEPDENGVIADFGRNRKMYIOAATSPKDVVILVDSGSMK 268
Db 267 -----GYFVHF---FAQGLPVY-----PKNIAFVIDVSGSMS 296
Qy 269 GLRLITAKQTVSSILDTGLDDDFNNILAYNEELHYEPCINGTLVQADRKKHFRHLD 328
Db 297 GRIQGTREALKILDDMEEDYLNFLSTGV---TWKDLVATPAPNLEAFAVYK 352
Qy 329 KL-----FAKGIGLIDALNDAFNIHSDFNHTGSGISCSQAIMITDGAVDYD 377
Db 353 NIDRSMNTNIDGLRGIEMLNKARED--HLVRS-----TSLVWLTTGDANTGE 402
Qy 378 TIFAKYNWDRKV--RIFTYLGREAFAADNLK---MACANGFFTOISTLADVOE 429
Db 403 SREKIQENVRNARIRKFKPLVNG---FGNNLVNPLESLAENHGFARIYEDSASL 458
Qy 430 NWEYIHLVSRPVVIDQHDVYVTEAYIDSTLTDGQPVLMITVAPVFSKQNETSKGI 489
Db 459 QLOGFYEEVAVP-----LLTNVEL----- 477
Qy 490 LIGVGADVPVKKELKTIPKYLGIYGAFATNNGIILHPELRLYEGRKKRRPNYS 549
Db 478 -----EYENAILD-----LTRNSI-----PHF- 495
Qy 550 SYDLSEWEDRDVDVLRNMAVNRKTKFSMEVKRYDKGRVLVMTNDYYTIDIKGTPFS 609
Db 496 -YDGESEI-----VAGRLVDRNVDFKADV----- 520
Qy 610 LGVALSRGRKTYFRGNVITIEBGLHDLHPDVLAD-----WSYCWTDLHPH 658
Db 521 -----GHAL--NDLFTTEEV--DMKEMDALKEOGYIFGDIYERLWAYLFR----- 562
Qy 659 RHLSQLEAIKLYLKGKPEPLLOCDELLQEVLPFAVVASAPIEAWTSTLAKSSENSDKGYE 718
Db 563 --IEQLLEKRNARQDE-----KENTTALALSLKYHVTPLTSKVVYKPPEDNEDQTA 614
Qy 719 VAFLGTRTGILSRINLFGVGAEQLTNODFLKAGDKENIFNADHPFLWYRRAAEQIPGS--FY 776
Db 615 IADKPEEALISASTAYLTSQ-----SSHSPLY--VDGDPHFH 651
Qy 777 YSIFSTGPVNSVNTASTSIQLDERKSPVAAV 812
Db 652 IQVP-----GKNDTICFN-----IDKPGTVLSLI 676
RESULT 14

BXG_CLOBO STANDARD: PRT: 1296 AA.

AC 060393:

DT 01-NOV-1997 (Rel. 35, Last Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

De Botulinum neurotoxin type G precursor (EC 3.4.24.69) (BONT/G)

De Botulinum neurotoxin type G precursor (EC 3.4.24.69) (BONT/G)

GN BONT.

OS Clostridium botulinum.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae; Clostridium.

OX NCBI_TaxID=1491;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=113 / 30;

RX MEDLINE=94092745; PubMed=8268233;

RA Campbell K., Collins M.D., East A.K.;

RT "Nucleotide sequence of the gene coding for Clostridium botulinum (Clostridium argentineense) type G neurotoxin: genealogical comparison with other clostridial neurotoxins."

RL Blochm. Biophys. Acta 1216:487-491(1993).

CC -1- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC NEURONS. IT INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC ENDOPEPTIDASE.

CC -1- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

CC -1- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY, WHILE THE N- AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL FORMATION AND TOXIN BINDING, RESPECTIVELY.

CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -1- MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF BOTULINUM NEUROTOXIN: TYPES A, B, C, D, E, F, AND G.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.

CC -----

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CC -----

DR EMBL: X71162; CA52275.1; -.

DR HSSP: P10845; 3BTA.

DR MEROPS: M27.002; -.

DR InterPro: IPR000395; Bontoxilysin.

DR InterPro: IPR000130; Zn_metallopep.

DR Pfam: PF01742; Peptidase_M27.1.

DR PRINTS: PR00760; BONTOKILYSIN.

DR PRODOM: PD001963; Bontoxilysin; 1.

DR PROSITE: PS00142; ZINC_PROTEASE; 1.

DR Neurotoxin: Hydrolyase; Metalloprotease; Zinc.

FT INT MET 0 BY SIMILARITY.

FT CHAIN 1 441 BOTULINUM NEUROTOXIN G, LIGHT-CHAIN.

FT CHAIN 442 1296 BOTULINUM NEUROTOXIN G, HEAVY-CHAIN.

FT METAL 229 229 ZINC (CATALYTIC) (BY SIMILARITY).

FT ACT_SITE 230 230 BY SIMILARITY.

FT METAL 233 233 ZINC (CATALYTIC) (BY SIMILARITY).

FT METAL 233 233 ZINC (CATALYTIC) (BY SIMILARITY).

FT DISULFID 435 449 INTERCHAIN (PROBABLE).

SO SEQUENCE 1296 AA; 149013 MW; DC8E47E15F65C31 CRC64;

Query Match 2.68; Score 146.5; DB 1; Length 1296;

Best Local Similarity 18.28; Pred. No. 0.29;

Matches 196; Conservative 172; Mismatches 397; Indels 313; Gaps 56;

43 KLV-ASAFGEIKSIAMKYSQLOKKYKKEKVAIEI-----DGLDLVKKLA 92

Db 345 KLYKALMGFTETNLAGEY-GIKTRYSESEYLPRIKTEKLLDNTIYQNEGFNIA-----S 400

Qy 93 KMEEMFHKKSFAVRVRLVDAEAEHLKH-----EPDADLOVEYF-----NALINERD-- 140

Db 401 KNLKTEFQNNKAVNK--EAAEISELHLVIYIRAMCKPVMKYKNGKSEOCITVNNEDLE 458

Qy 141 ----KDGNELELGEKFIAPNDHFNNLPVNISL-----SDVQV---TNNYKNDP 183

Db 459 FIANKDSFKDLAKETIATNTQNTIENNFISDILLDNDLSSGIDLPENETFEPTAND 518

Qy 184 AIVNGVWSES-LNKVPVNDPDRPSLIWQYFGSAKGFROYGKWEPPDENGVIAPDCR 242

Db 519 DIDIPVIYIKOSALKRIFVDG-----DSLFEYL-HAQTFPSNIENQLTNSLDALR---N 569

Qy 243 NKKWVIQATSPKDVILLVDVSGSMKGLRLT-----AAQVYSILDTIGDDDF 291

Db 570 NKKVYTFPSTN-----LVEKANTVYGASLFVNWVKYVIDFTSSTQSTIDKVS--- 620

Qy 292 FNIIAYNEELHYVEPCLNTLQADRTNKEHREHLN-----KLFAKGIQMDIALNEAFN 347

Db 621 VSII-----IPYIGALN-----VGNETAKENKNAFELGGAAILMEFIPELVPTVGFET 671

Qy 348 ILSDFNHTGGGSGISQAILMLTIDGAVDVTYDTIYAAYNMPDRKRVLTFTYLIGREAAFDNL 407

Db 672 LESYGNKNGH-----IIMTISNALKRRD-----QKWTD---MYGLIVS----- 706

Qy 408 KIMACANKGFTQISTLADVOENVMELHYLVS--PKYIDQEHVDVWVTEAYIDSTLTDDQ 465

Db 707 QMLSTVNTQFYT-----IKRMYNALNLOSQALEKIIEDQYNNRSEEDKINIID--- 756

Qy 466 GPVLNTTVAAMPFSKONETRSKILLGVGVD-----VPYKELKTIPT 508

Db 757 -----FNIDFKRLNSILAINNIDDFINQCSISYLNMRMPLAVKAKLKDD 804

Qy 509 KYKLGIGAFATITNGGILTHPELRLLYEGSKRRKPNYSVDSEVEMEDRDVYRNA 568

Db 805 NLKRLLEY-IDTIELYLL--DEVNIIKSKVRHLKOSI--PFDLS---LYTKDILLQV 856

Qy 569 MVRKRTKFSMEVKTKVQSKRLVMT-----NYYIYDITGTFPSLGVALSRRGH 619

Db 857 FNNYISNISNAITLSIRGRLIDSSGATMNVGSDVTFNDINQFKLNSEN----- 912

Qy 620 KYFFGNVYIEG--LHDLHPDVSLADEMS-----YCNTDLPHERHLSQLEAI 667

Db 913 ----SNTFAHQSKRVYVD-----SMFDNFSINFWVTPKRYNNND-----I 948

Qy 668 KLYLKGEPLOCKELIQEVLFDVAVSAPIEA---YTSIALNKSENS----- 713

Db 949 QTYLQNEFTIISCIN-----DSGMWVYSIKGNRIIMTLIDVNAKSKSIFEYSIKONI 1001

Qy 714 ----DKGEVAFELGRTGSLRINLVGAEQLTNOEFLAGDKENFENDHPL----- 762

Db 1002 SDYINKWFSITTYNDRLG--NANIYIINSLKXSEIILNL--DRINSSNDIDKRLINCTDTT 1058

Qy 763 ---W-----YRAAEQIIPGSEFVSIPESTGPVKN--SNVYASTSIQULDERKSPV-- 809

Db 1059 KFWVWKDFNINIGRELATNEVSSLYIGSTNTMLKPFQWGNPLKRYDQYVLLPQNGQNIYIK 1118

Qy 810 -----AAVGIO---MKLEFQKRFATSHQCSALDGKCSISCD-- 845

Db 1119 YFSKASMGETAPRTNNAANAYONLVLGLRFLIK-----ASNSRINNDNIYR 1168

Qy 846 ETVNGYL-IDN-----NGFLVYSDYIQTQDFFGEI--EGAVMNKLLLMGSKRRTLLDY 897

Db 1169 EGDYIYLLNIDSDSESYVYVVLVNSKEITOTQLAPINDPPEYDQVLDIKKYEYKTYTNC 1228

Qy 898 QAMCRANKESSDGAHGL-----LDPYNAFLSAVKWIMTELVLVLFVEFNL--CSW 944

Db 1229 QILCKDKTKTF--GLFGICKFVKDGYVMDYTDNFCISQWILRRISEININRLRLGCMW 1285

RESULT 15

.....

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 16, 2002, 22:18:00 ; Search time 117.99 Seconds

(without alignments)
1590.809 Million cell updates/sec

Title: US-09-787-657-5

Perfect score: 5667
Sequence: 1 MAGPGSPRRASRGASALIAA.....SLQAQTVLLPLLMLEFSR 1085

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_plant:*
10: sp_rodent:*
11: sp_virus:*
12: sp_vertebrate:*
13: sp_unclassified:*
14: sp_virus:*
15: sp_bacteriap:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5524	97.5	1091	11	Q9Z1L5
2	5198	91.7	997	4	Q9NY16
3	2600	45.9	519	4	Q9NY18
4	1409.5	24.9	2190	5	Q9NK64
5	1394.5	24.6	2172	5	Q9VJMO
6	1382.5	24.4	1022	5	Q9V6T7
7	1376.5	24.3	1191	5	Q9VJN7
8	1374.5	24.3	1235	5	Q9NK83
9	1209.5	21.3	1150	4	Q9NY47
10	1209	21.2	1143	4	Q9NY48
11	1200	21.0	1076	4	Q9Y268
12	1188.5	20.9	1156	11	Q9E0G2
13	1183.5	20.8	1084	11	Q9Z0H6
14	1181	20.6	1103	11	Q08532
15	1168.5	20.4	1091	11	Q9ERS3
16	1157.5	20.4	1091	11	Q9ERS3

17	1151.5	20.3	1091	6	077773	077773 sus scrofa
18	1134	20.0	1110	4	Q9UIU0	Q9UIU0 homo sapien
19	1093	19.3	975	4	Q9NSA6	Q9NSA6 homo sapien
20	987.5	17.4	842	5	Q95R75	Q95R75 drosophila
21	899	15.9	180	6	Q9GMV4	Q9GMV4 macaca fasc
22	678.5	12.0	745	4	Q9UDQ3	Q9UDQ3 homo sapien
23	561	9.9	1148	5	017517	017517 caenorhabdit
24	365	6.4	317	11	Q920H5	Q920H5 mus musculus
25	335.5	5.9	170	4	Q9UDL7	Q9UDL7 homo sapien
26	320.5	5.7	1185	4	Q9HCJ9	Q9HCJ9 homo sapien
27	206	3.6	1449	5	Q9V917	Q9V917 drosophila
28	203	3.6	1450	16	Q9CE07	Q9CE07 lactococcus
29	189	3.3	978	6	Q95KE0	Q95KE0 macaca fasc
30	178	3.1	100	6	Q9GLH1	Q9GLH1 bos taurus
31	163.5	2.9	886	11	Q91K69	Q91K69 mus musculus
32	162.5	2.9	223	11	Q91K42	Q91K42 mus musculus
33	161.5	2.8	1577	5	Q9NKC7	Q9NKC7 drosophila
34	159.5	2.8	946	6	Q9GLY6	Q9GLY6 oryctolagus
35	153	2.7	2166	16	051465	051465 borrelia bu
36	151.5	2.7	907	13	Q9PVP8	Q9PVP8 brachydanio
37	146	2.6	532	2	Q9L1J5	Q9L1J5 streptomyce
38	145.5	2.6	3254	5	Q9BK45	Q9BK45 plasmodium
39	144.5	2.5	4081	5	Q9VWZ3	Q9VWZ3 drosophila
40	141.5	2.5	525	4	076057	076057 homo sapien
41	140.5	2.5	1159	2	P71109	P71109 clostridium
42	140	2.5	1387	5	Q9GZ76	Q9GZ76 plasmodium
43	139.5	2.5	903	6	Q9GLY5	Q9GLY5 oryctolagus
44	139.5	2.5	906	6	Q9TJ04	Q9TJ04 oryctolagus
45	139.5	2.5	1302	2	Q49547	Q49547 mycoplasma

ALIGNMENTS

RESULT 1
ID Q9Z1L5 PRELIMINARY: PRT: 1091 AA.
AC Q9Z1L5:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CALCIDIUM CHANNEL ALPHA-2-DELTA-C SUBUNIT.
GN CACNA2D3.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Klugbauer N., Lacinova L., Marais E., Hobom M., Hofmann F.;
RT "Molecular diversity of the calcium channel alpha2delta subunit.";
RL J. Neurosci. 19:648-691(1999).
DR EMBL: AJ010949; CAA09423.1; -
DR MGD: MGI:1338890; Cacna2d3.
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; VMFA.
DR Pfam: PF02743; Cache; 2.
DR SMART: SM00327; VWA; 1.
DR PROSITE: PS50234; VMPA; 1.
SO SEQUENCE 1091 AA; 122777 MW; 7AE2BDAL0077A0A CRC64;

Query Match 97.5%; Score 5524; DB 11; Length 1091;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 1064; Conservative 2; Mismatches 19; Indels 6; Gaps 1;

QY 1 MAGPGSPRRASRGASALIAALTYALGIVRSSEOIPISTVTKMSARGGEIKTSIAAY 60
Db 1 MAGPGSLCCASRGASALIALTALTYALGIVRSSEOIPISTVTKLWASAFGEIKTSIAAY 60
QY 61 SCSQLQKKYKEKDVAAIEEIDGLVKKLAKNMEEMFHKRSEAVRRIVEAAEHLKH 120
|||||

Db 61 SGSQLKKKYEKEKDAIEEIDGLQVKKLAKIMEEHHKSEAVRRLEAVEAEHLKH 120
OY 121 EFDADLOEYENAVLINERDKGNFLELGKEPILAPNDHPNNLPVNISLSDVQVPTNNYN 180
Db 121 EFDADLOEYENAVLINERDKGNFLELGKEPILAPNDHPNNLPVNISLSDVQVPTNNYN 180
OY 181 KDAIIVNGVWSESINKVFNDFRPSLIQWFGSAGKFFRQYPGIIMEPDENGVIAPD 240
Db 181 KDAIIVNGVWSESINKVFNDFRPSLIQWFGSAGKFFRQYPGIIMEPDENGVIAPD 240
OY 241 CRNRKWTIOAATSPKDVYILVDVSGSMKGLRTIAKOTVSSLDLTGDDDFNNITAYNEE 300
Db 241 CRNRKWTIOAATSPKDVYILVDVSGSMKGLRTIAKOTVSSLDLTGDDDFNNITAYNEE 300
OY 301 LHAYEPCNLGLVQADPTNKEHFRHLDBLKFAKIGMDILNEAFNLLSDPNHNGGCSI 360
Db 301 LHAYEPCNLGLVQADPTNKEHFRHLDBLKFAKIGMDILNEAFNLLSDPNHNGGCSI 360
OY 361 CSQAIMLTIDGAVDTYDTIFAKYKMPDRKVRIFTYLLIGREAAFDNLKMACANKGFFTO 420
Db 361 CSQAIMLTIDGAVDTYDTIFAKYKMPDRKVRIFTYLLIGREAAFDNLKMACANKGFFTO 420
OY 421 ISTLADVOENMEYLVHSRKPVIDOEHDVWTEAYIDST-----LTDGCPVLTMTVA 474
Db 421 ISTLADVOENMEYLVHSRKPVIDOEHDVWTEAYIDST-----LTDGCPVLTMTVA 474
OY 475 MPVFSKQNETRSKGLLGCVGTDPVKELTKTIPKYLIGYAFATINNGYILTHPELR 534
Db 475 MPVFSKQNETRSKGLLGCVGTDPVKELTKTIPKYLIGYAFATINNGYILTHPELR 534
OY 535 LLYEGRKKRRPNVSSVDLSEVEDRDLVLRNANVRKTKGFSMEVKKTYDKGRVLVM 594
Db 535 LLYEGRKKRRPNVSSVDLSEVEDRDLVLRNANVRKTKGFSMEVKKTYDKGRVLVM 594
OY 595 TNDVYNDIKCTPSPSLGALSRRGCKYFFRGVNTIEEGLHLEHFDVSLADEMSKCNLD 654
Db 595 TNDVYNDIKCTPSPSLGALSRRGCKYFFRGVNTIEEGLHLEHFDVSLADEMSKCNLD 654
OY 601 TNDVYNDIKCTPSPSLGALSRRGCKYFFRGVNTIEEGLHLEHFDVSLADEMSKCNLD 660
Db 601 TNDVYNDIKCTPSPSLGALSRRGCKYFFRGVNTIEEGLHLEHFDVSLADEMSKCNLD 660
OY 655 HPEHRHLSQLEAIKLYLKGEKPELLOCEKLEOEVLFDVAVSAPIPAYWTSIALNKSEMSD 714
Db 655 HPEHRHLSQLEAIKLYLKGEKPELLOCEKLEOEVLFDVAVSAPIPAYWTSIALNKSEMSD 714
OY 661 HPEHRHLSQLEAIKLYLKGEKPELLOCEKLEOEVLFDVAVSAPIPAYWTSIALNKSEMSD 720
Db 661 HPEHRHLSQLEAIKLYLKGEKPELLOCEKLEOEVLFDVAVSAPIPAYWTSIALNKSEMSD 720
OY 715 KGEVAELGRTGTGLSRINLFGAEOLTNQDFLKAAGDKENIFNADHPLMYRRAAEQIPGS 774
Db 715 KGEVAELGRTGTGLSRINLFGAEOLTNQDFLKAAGDKENIFNADHPLMYRRAAEQIPGS 774
OY 721 KGEVAELGRTGTGLSRINLFGAEOLTNQDFLKAAGDKENIFNADHPLMYRRAAEQIPGS 780
Db 721 KGEVAELGRTGTGLSRINLFGAEOLTNQDFLKAAGDKENIFNADHPLMYRRAAEQIPGS 780
OY 775 FVYSIPSTGTGVNKSNNVTASTSTQILDERKSPVAAVGIOMKLEFPQRKFWTASROCAS 834
Db 775 FVYSIPSTGTGVNKSNNVTASTSTQILDERKSPVAAVGIOMKLEFPQRKFWTASROCAS 834
OY 781 FVYSIPSTGTGVNKSNNVTASTSTQILDERKSPVAAVGIOMKLEFPQRKFWTASROCAS 840
Db 781 FVYSIPSTGTGVNKSNNVTASTSTQILDERKSPVAAVGIOMKLEFPQRKFWTASROCAS 840
OY 835 LDGKCSISDDEETVNCYLIDNNGFLVSESDYTGTFGGEIEGAVMNKLLTMGSPKRTTL 894
Db 835 LDGKCSISDDEETVNCYLIDNNGFLVSESDYTGTFGGEIEGAVMNKLLTMGSPKRTTL 894
OY 841 LDGKCSISDDEETVNCYLIDNNGFLVSESDYTGTFGGEIEGAVMNKLLTMGSPKRTTL 900
Db 841 LDGKCSISDDEETVNCYLIDNNGFLVSESDYTGTFGGEIEGAVMNKLLTMGSPKRTTL 900
OY 895 YDYOAMCRANKESSDGAHLLDPYNAFLSAVKWINTLVLFLVEBNILCSMMHSDMTAKAQ 954
Db 895 YDYOAMCRANKESSDGAHLLDPYNAFLSAVKWINTLVLFLVEBNILCSMMHSDMTAKAQ 954
OY 901 YDYOAMCRANKESSDGAHLLDPYNAFLSAVKWINTLVLFLVEBNILCSMMHSDMTAKAQ 960
Db 901 YDYOAMCRANKESSDGAHLLDPYNAFLSAVKWINTLVLFLVEBNILCSMMHSDMTAKAQ 960
OY 955 KLKQTLERPCOTREYPAFVSERTIKETGTGNIACEDCSKSFVIOQIPSSNLFMVVSSSCICE 1014
Db 955 KLKQTLERPCOTREYPAFVSERTIKETGTGNIACEDCSKSFVIOQIPSSNLFMVVSSSCICE 1014
OY 961 KLKQTLERPCOTREYPAFVSERTIKETGTGNIACEDCSKSFVIOQIPSSNLFMVVSSSCICE 1020
Db 961 KLKQTLERPCOTREYPAFVSERTIKETGTGNIACEDCSKSFVIOQIPSSNLFMVVSSSCICE 1020
OY 1015 SVAITMAPIRIRYNESLCKERLKAOKIRRRPESCHGHPENARECGGASLOAQVTL 1074
Db 1015 SVAITMAPIRIRYNESLCKERLKAOKIRRRPESCHGHPENARECGGASLOAQVTL 1074
OY 1021 SVAITMAPIRIRYNESLCKERLKAOKIRRRPESCHGHPENARECGGASLOAQVTL 1080
Db 1021 SVAITMAPIRIRYNESLCKERLKAOKIRRRPESCHGHPENARECGGASLOAQVTL 1080
OY 1075 LPLLLMLFSR 1085
Db 1075 LPLLLMLFSR 1085
OY 1081 LPLVSSLSFR 1091
Db 1081 LPLVSSLSFR 1091

ID O9NY16 PRELIMINARY; PRF: 997 AA.
AC O9NY16;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 15, Last annotation update)
DE CALCIUM CHANNEL ALPHA2-DELTA3 SUBUNIT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=21142395; PubMed=11245980;
RA Hanke S., Bugert P., Chudek J., Kovacs G.;
RT "Cloning a calcium channel alpha2delta-3 subunit gene from a putative
RT tumor suppressor gene region at chromosome 3p21.1 in conventional
RT renal cell carcinoma.";
RL Gene 264:69-75(2001).
DR EMBL; AJ272268; CAB75962.1; -
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; WFA.
DR Pfam; PF02743; Cache: 2.
DR SMART; SM00327; WFA; 1.
DR PROSITE; PS50234; WFA; 1.
SQ SEQUENCE 997 AA: 112996 MW: 856D1313FD678BD CRC64;

Query Match 91.7%; Score 5198; DB 4; Length 997;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 991; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

OY 95 MEEMFKKSEAVRRIRVEAAEAEHLKHEFDADLOEYFNAVLINERDKGNFLELGKEPIL 154
Db 1 MEEMFKKSEAVRRIRVEAAEAEHLKHEFDADLOEYFNAVLINERDKGNFLELGKEPIL 60
OY 155 APNDHFNMLPVNISLSDVQVPTNMYNKDPAIVNGVWSESINKVFNDFRDPSPLIQWYF 214
Db 61 APNDHFNMLPVNISLSDVQVPTNMYNKDPAIVNGVWSESINKVFNDFRDPSPLIQWYF 120
OY 215 GSAKGFQYQYGIKKEPDENGVIAFDCCNRKRYIOAATSPKDVYILVDVSGSMKGLRTLI 274
Db 121 GSAKGFQYQYGIKKEPDENGVIAFDCCNRKRYIOAATSPKDVYILVDVSGSMKGLRTLI 180
OY 275 AKOTVSSILDTLGDGDDFNIIAYNEELHYVEPCLNGTLVQADRTKKEHFRHLDBLKFAKG 334
Db 181 AKOTVSSILDTLGDGDDFNIIAYNEELHYVEPCLNGTLVQADRTKKEHFRHLDBLKFAKG 240
OY 335 IGMIDLALNEAFNLLSDPNHNGGGSICQAIMLTIDGAVDTYDTIFAKYKMPDRKVRIFT 394
Db 241 IGMIDLALNEAFNLLSDPNHNGGGSICQAIMLTIDGAVDTYDTIFAKYKMPDRKVRIFT 300
OY 395 YLIGREAFADNLKMACANKGFFTOISTLADVOENMEYLVHSRKPVIDOEHDVWTE 454
Db 301 YLIGREAFADNLKMACANKGFFTOISTLADVOENMEYLVHSRKPVIDOEHDVWTE 360
OY 455 AYIDST-----LTDGCPVLTMTTAAVPFSKONETRSKGLLGAVGADVPVKELTKTIP 508
Db 361 AYIDSTLQAOAKLTDGCPVLTMTTAAVPFSKONETRSKGLLGAVGADVPVKELTKTIP 420
OY 509 KYKLGINGAYATINNGYILTHPELRLLYEBGKRRKPNVSSVDLSEVEDRDLVLRNA 568
Db 421 KYKLGINGAYATINNGYILTHPELRLLYEBGKRRKPNVSSVDLSEVEDRDLVLRNA 480
OY 569 MVNKRKTGFSMEVKKTYVKGKRVLMYNTDYTTDKGTPESLGAVALSGHGKYPFRGAVT 628
Db 481 MVNKRKTGFSMEVKKTYVKGKRVLMYNTDYTTDKGTPESLGAVALSGHGKYPFRGAVT 540
OY 629 IEEGLHLEHFDVSLADEMSKCNLDLHPEHRHLSQLEAIKLYLKGEKPELLOCEKLEOE 688
Db 541 IEEGLHLEHFDVSLADEMSKCNLDLHPEHRHLSQLEAIKLYLKGEKPELLOCEKLEOE 600
OY 689 LFDVAVSAPIPAYWTSIALNKSENSDKGEVAELGRTGTGLSRINLFGAEOLTNQDFLKA 748

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Db 1 JEDAVVASPIEAWTSLANKSENDSKGEVAFLTGRGLSLNLFVGAEOJLNDFLKA 660
Qy 749 GDKREIFNADHPPLMYRRAAEOIPGSFYIPIFSTGPVKNKSVVASTSIQLDERKSPV 808
Db 661 GDKREIFNADHPPLMYRRAAEOIPGSFYIPIFSTGPVKNKSVVASTSIQLDERKSPV 720
Qy 809 VAAVGIOMKLEFFORKFMTASROCASLDGKCSISCDDEFVNCYLLIDNNCFILVSEDTYT 868
Db 721 VAAVGIOMKLEFFORKFMTASROCASLDGKCSISCDDEFVNCYLLIDNNCFILVSEDTYT 780
Qy 869 GDFEIGEIGAVANNKLLTNGSEFRITLYDQAMCRANKESSDGAHGLDPEYNAFLSAVKVI 928
Db 781 GDFEIGEIGAVANNKLLTNGSEFRITLYDQAMCRANKESSDGAHGLDPEYNAFLSAVKVI 840
Qy 929 MTELVLFLVEFNLCGSMWHSMDMTAKAKQLKOTLEPCDTEYPAFVSERTIKETGINIACEDC 988
Db 841 MTELVLFLVEFNLCGSMWHSMDMTAKAKQLKOTLEPCDTEYPAFVSERTIKETGINIACEDC 900
Qy 989 SKSEFVIOQIPSSNLFPMVVDSCLESVAPIPMAPLEIRYNSLCCERLKAQIRRPES 1048
Db 901 SKSEFVIOQIPSSNLFPMVVDSCLESVAPIPMAPLEIRYNSLCCERLKAQIRRPES 960
Qy 1049 CHGFPEENARECGAPSLQAOVTVLLPLMLFSR 1085
Db 961 CHGFPEENARECGAPSLQAOVTVLLPLMLFSR 997

RESULT 3
Q9NY18 PRELIMINARY: PRT: 519 AA.
AC Q9NY18:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CALCIUM CHANNEL ALPHA2-DELTA3 SUBUNIT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=21142395; PubMed=11245980;
RA Hanke S., Bugert P., Chudek J., Kovacs G.;
RT "Cloning a calcium channel alpha2delta-3 subunit gene from a putative
RT tumor suppressor gene region at chromosome 3p21.1 in conventional
RT renal cell carcinoma.";
RL Gene 264:69-75(2001).
DR EMBL: AJ272213; CAB75878.1; -
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; VWFA.
DR Pfam: PF02743; Cache: 1.
DR SMART: SM00327; VMA; 1.
DR PROSITE: PS50234; VWFA; 1.
SQ SEQUENCE 519 AA; 59526 MW; 198D13AF246286C6 CRC64;
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Qy 275 AKOTVSSITLDTGDDDFENFIAYNEELHYVEPLCNGTLVOAQRNKNREHREHDLKFLAK 334
Db 181 AKOTVSSITLDTGDDDFENFIAYNEELHYVEPLCNGTLVOAQRNKNREHREHDLKFLAK 240
Qy 335 IGLDIALNEAFNLSDFNHTGSGISCSOAIMLTIGAVDYDTIPAKYNMPDRKRIPT 394
Db 241 IGLDIALNEAFNLSDFNHTGSGISCSOAIMLTIGAVDYDTIPAKYNMPDRKRIPT 300
Qy 395 YLIGREAPADNLKMACANKGFTQISTLADVOENVMEXLHLSRPKYIDOEHDVWTE 454
Db 301 YLIGREAPADNLKMACANKGFTQISTLADVOENVMEXLHLSRPKYIDOEHDVWTE 360
Qy 455 AYIDSLTLDQGGVLTMTYAMPVFSKONETRSKGLLVGVDVPRKELKTIPKYLGI 514
Db 361 AYIDSLTLDQGGVLTMTYAMPVFSKONETRSKGLLVGVDVPRKELKTIPKYLGI 420
Qy 515 HGAFATNNGYLLTPELRLYEKGKRRKPYSSVDSLEVEDRDVLRNANVRKT 574
Db 421 HGAFATNNGYLLTPELRLYEKGKRRKPYSSVDSLEVEDRDVLRNANVRKT 480
Qy 575 GKFSMEVKKTVDKGR 590
Db 481 GKFSMEVKKTVDKGR 496

RESULT 4
Q9NR64 PRELIMINARY: PRT: 2190 AA.
AC Q9NR64:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE HYPOTHETICAL 249.8 KDA PROTEIN.
GN BG:DS07473.1 OR CG12455.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyroidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Mitra S., Roote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzeil G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
RA Celniker S., Rubin G.M.;
RT "An exploration of the sequence of a 2.9-Mb region of the genome of
RT Drosophila melanogaster: the Adh region.";
RL Genetics 153:179-219(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;
RA Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA Butenhof C., Champe M., Chavez C., Chew M., Ciesioika L., Doyle C.M.,
RA Farfan D.E., Galle R., Humastil S.R., Kaira K., Kearney L., Kim E., Lee B.,
RA Houston K.A., Humastil S.R., Kaira K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomtan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Smit E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zietan L.L., Rubin G.M.;
RL Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE003415; AAF44988.1; -
DR FlyBase: FBgn0028859; BG:DS07473.1.
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; VWFA.
DR Pfam: PF02743; Cache: 1.
DR SMART: SM00327; VMA; 1.
DR PROSITE: PS50234; VWFA; 1.
KW Hypothetical protein.
SQ SEQUENCE 2190 AA; 249754 MW; B8C657A2F80F226E CRC64;
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DR InterPro: IPR004010; Cache.
 DR InterPro: IPR002035; vMFA.
 DR Pfam: PF02743; Cache; 2.
 DR SMART: SM00327; vMA; 1.
 DR PROSITE: PSS00234; vMFA; 1.
 SO SEQUENCE 1022 AA; 117842 MW; 85F2223305D4F56F CRC64;

Query Match 24.4%; Score 1382.5; DB 5; Length 1022;
 Best Local Similarity 31.1%; Pred. No. 1,3e-83;
 Matches 335; Conservative 183; Mismatches 333; Indels 225; Gaps 26;

150 KEETIAPNDHFNPLPVNISLSDVOVPTNMYNKDPAIVNGVYMSLNKYPVDFDRDPSL 209
 15 KVVLEPRREFHNTPVNFSSVHVHVNDRAVDVIAIKAIOMSENIDQIFRDYKNDPDL 74
 210 INQFESAGFFRQPGIKWEPDENGVIAPDCNRKRYIOAISPFDVYLIVSSGSMK 269
 75 SMOFSSSTGFMQFPASKWRKV-DVLDYDCRLRSWMEAAATSPKDIYILMDGSGSMLG 133
 270 LRLTIKQTVSSILDTLGDDEFNIIVAYNEELHYVEPCLNGTLVQADRTEKEHREHLDK 329
 134 QRLDIKHHVNTLDTLGNDFNITFDKEVSPVPCEDTLIQANLGNIRLEKIGEL 193
 330 LRAKIGIMDIALNEAFNILDSPNHTGSGISQAIIMLTGDAVDYDTIFAKYNN--P 386
 194 FRPKSIANTYALTAKAFELLEETKLSRGAOCQAQIAIITIGDGAPENNREVEFLHNRDP 253
 387 DRKRVETFLIGREAFADNLKMACANKGEFQISTLADVOENWMEYLHVSRLPVIDQ 446
 254 YKRVRFVTLIGKEVANNMDIRMACENOGYVHLSDTAEVRMVLNYPVMAKPLVLR 313
 447 -EHDVWTEAYI--DSTLDT-----DQGPLY----- 469
 314 HHHPVMSQVYADIEDTKLSDYIMDINOCEYKADYLEWQVHDMLEPSEMRKRYRM 373
 470 -----MTVAMPYFS-KONETRSKIGLLGVGTDPVKELKTIPYKYLK 513
 374 KETWNPQVSNVYQFMTYTSMPYDRRENATRIANI-LGAGTGDVINEIKTLLSPF--- 429
 514 IGVAFATNNNGYILTHPELRLLYEEGKKRRKPNSSVSLSEVEMDRDVLNNANVRK 573
 430 -----TFQGYIL-----KPAVSYDMIEELLDDDPADP----- 460
 574 TGRFSMEVKKTVKGRKVLMTNDYYTIDIKTFESLGVALSFGHSGHYFEGNVTIEGL 633
 461 -----NPVLMTRVARVRKQYYWTAIKKTFPLVLSYRQYGVSHM--DIRADQEL 509
 634 HLEHNPVSLADEWSTCNTDLHPE-----HRHLS-----OLEAIKLYLKGEK- 676
 510 HRIISIKGTMLRSVFGSKRWKIHDPDLCFKHSNRTFKTPEIETLLYFLERMSEPGMRPGSR 569
 677 -----LLOCDKEILIOEVLDAVVASPIEAYWTSLLANKSENSDK-----GVEY 719
 570 SAMPRPAAAMCDROLMALVFDARVGTG-----WFSNNTSFKSKDKGNEFKQREGVTV 624
 720 AFLGRTGSLSRINLF-----VGAEOLTNODFLKAGDENENFNADHPFLMYRRAEO-- 770
 625 AFLATHSGLTIRHHEFHNSNAEESGVEFSSQNNTRAIDE-----IWKRAVDQHF 674
 771 -IPGSEVYSIPSTGCPYVKSNNVYVASTIQLLDERKSPVAVAVGIOKLEFPQKRWAS 829
 675 VREESVYSVPPDAGSENSIELVTASHAVFHNEGKTAAPAAYVGFQFOSALYKLEFHNT 734
 830 RQCASLDGCSISCODETYNCLINNGFLIYSEDYTOGDFEGELEGVNMKLLTMSGF 889
 735 GNACAVDDK-----DCYTLIDNNGYVILSTRVHEGFRFEGVNGAIMKRLLEENVY 784
 890 KRITLYDQAMRANKESSDGAHGLDPYNAFLSAVKWIMTELVELVLFVFNLCSM----- 944
 765 RQVYVYDQAVCFESKNDNNASSMLSLPLFHLIRYKGLWILHRAKTYIV--LLQANPGVS 842
 945 -----WHSDMTAKAKLKLQTELEPCT 965

DB 843 SHYADMGDSNDTEPPPEPPHDPHHAANGHGKKDDHMLRYTLHTRTLK-----PCDM 898
 QY 966 EYPAFVSERIKETKTGIAECDESKSVIOQITSSNLFMYVNVSSCLCEVAITAPRIE 1025
 DB 899 KDLTYTLFNEKDNVNMVMTNAHAERPFVPLPIPFSSNILLVLIQDLCPDSDSVVLTVP 958
 QY 1026 IRY-----NESLACERLKAOKIRRRPESCHGFHEENA-RECGGAPSLQAOVTVLLL 1076
 DB 959 IDHLSVNSDLACYKQAKREFRMRPHPSICSRHANSIGIKLCGACSVYANLGLLLL 1014
 RESULT 7
 Q9VJN7
 ID Q9VJN7 PRELIMINARY: PRT: 1191 AA.
 AC Q9VJN7:
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
 DE BG:DS07108.2 PROTEIN.
 GN BG:DS07108.2 OR CG4587.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertman B.P., Bhargava D., Bolshakov S.,
 RA Borova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burks K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Danike C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertler S., Fleischmann W.,
 RA Foster J.C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Lasro P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merulov G., Milshina N.V., Modarres C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazozo M., Pittman G.S., Pan S., Pollard J., Puvi V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weisslock G., Wu D., Yang S., Yao Q.A.,
 RA Williams S.M., Woodard T., Worley K.C., Xu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003648: AAF53476.1;
 DR FLYBASE: FBgn0028863; BG:DS07108.2.
 DR InterPro: IPR004010; Cache.
 DR InterPro: IPR002035; vMFA.
 DR Pfam: PF02743; Cache; 1.


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Db 382 LQNSNITRAN--CNKIMMFTDGEDRDVDVEKYNMPPRTVTFEFGQINIDVTPIQ 439
Oy 409 WMACANKGEFTQISTLADVOENMEYLHLSRPKYI--DOEHVYVTEAYIDSTLTDDG 466
Db 440 WMACANKGYEPEIPISGIRINTOEYLDVGRPMVLAGEAKQVOMTNYEDAL-----G 494
Oy 467 PYLMTVAMPVES-----KONETRSKGILLGVGTDVPVKELTKTPKXKLGICGYA 518
Db 495 LGLVVTGTLPEVFNLTQDGEKKNO-----LILGVMGIDVALNDIKRLTPNTTLGANGV 549
Oy 519 FAITNNGYILTHPELRLLYEEGKRRKPNYSVSDSEVEMEDRDVLFNANMNRKTGKS 578
Db 550 FAIDNGVYLHLPNK-----POTTNPREVYTDLPDALEDEKEETIRSMIDONKCHKQI 606
Oy 579 MEVKTVDKGRKVLVMTNDYYTIDIGTPFSLGVALSRGKGFFRGVNTIE----- 630
Db 607 RTLYVSLDE--RYIDEVTRNTVWPIRSTNYSGLVLP--PYSTFYLOANLSDQILQVKLRI 664
Oy 631 EGIHLE-----HPDVLADMSYCNDLHPEHRLSLE-AIKLYLKGKEPLQOC 680
Db 665 SKLKFEFLDBSFESEGHVFIAPR-ERYCK-DLNASDNNTEFLKMFILMEKVTDPDSKQC 722
Oy 681 DKELIOEVLFD-AVVSADIEAYWTSLALNKSSENSDKGEVAFIAGRTGLSRINLFGVAGQ 739
Db 723 NNFLHNLILDTGITOQLVERVMRQODLN-----TYSLLAVFAATDGTITRVFPNKAED 777
Oy 740 LTNOFLKAGDKENIFNADHPELWYRAAEQIPGSEFVYSIPESTG--PVNKS--VVT 793
Db 778 WT-----ENRPEPFNS--FYRSLDN--HGIVFEPHQDALLRPLELENDVTGIL 823
Oy 794 ASTIQLDERKSPVAAVGIOMKLEFPORKWTAS-----RQASLDGKCSISD 844
Db 824 VSTAELSILGRTLPRAVAVGVKLDEMAAEKKVVLASNRTMODOPQKGP-MSHCMEDE 882
Oy 845 --DETNYCYLIDNNGFIYVS--EDYTQDGFEGIEGAVNMKLTJMSFKRTTYLDYOA 899
Db 883 VNNEELLVLIDDGFFVLVSNQNHQMDVGRFSEVDATLALINNAYTTTKESTIDYA 942
Oy 900 MCRANKESDGA--HGLLDIPYNA-----FLSAVKWIMTELVLFLVEFNLCSMWHSMT 950
Db 943 ACAPOPGNLGAAPRGVFPVADFLNLAMWTSAAAMSFLQQLGLIYH--SMFOAD-P 999
Oy 991 AKAQKLTLEPCDTEYFAFVSERTIKET-----TGNICEOSKSFVLOQIPS 999
Db 1000 AEABESPETRE-----SSCVMKQTOYVFGSVMSYNAIIDCGNCSRLFHQRLTN 1049
Oy 1000 SNLFMVVVDSCICESVAPITWAPIEIRYNESLKCERLKAOKIRRRPESCHGFPEENAR 1059
Db 1050 TNLFLVFAKEP-LCSQCEAGRLLOKETHSDGPEOCELVORPPRYRGFHCIPDYMNATEDIS 1108
Oy 1060 ECG-GAPSLQAOQTVLLPLPLML 1082
Db 1109 DCGRGASFPFSLGLVLSQLLILL 1132

RESULT 10
O9NY48 PRELIMINARY; PRT: 1143 AA.
AC O9NY48:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE CALCIUM CHANNEL, ALPHA 2/DELTA SUBUNIT 2.
GN CACNA2D2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA Klugbauer N.;
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RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
RP [2]
RN SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA Hobom M., Dai S., Marais E., Iachnova L.;
RT "Neuronal distribution and functional characterization of the calcium
RT channel alpha2delta-2 subunit.";
RL Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ251367; CAB86192.1; -.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; WFA.
DR Pfam; PF02743; Cache; 1.
DR SMART; SM00327; WFA; 1.
DR PROSITE; PS0234; WFA; 1.
SQ SEQUENCE 1143 AA; 129085 MW; 492556C9919A0CE5 CRC64;

Query Match 21.3%; Score 1209; DB 4; Length 1143;
Best Local Similarity 29.7%; Pred. No. 6, 1e-72;
Matches 344; Conservative 222; Mismatches 452; Indels 140; Gaps 41;

Oy 3 GPGSPRRAS--RGASALLAALLVYALGDVYRSEDOQIPLSVYKIMASAFGEIKSIATK 59
Db 30 GPGTRRPTSGPRPLMLPLPLPLAAGSAYSFPO--QHTQHWARRLEQEVGDMRI 87
Oy 60 YGSQLQKKKYEKDVAEIDIGLQVKKLAKNEMEPHKSEAVRLVEAEBAHLK 119
Db 88 FGVOQLREITYKDNRLMEFVENEPQKLVKGVAGDIESLDRVQALKRLADAENFQKA 147
Oy 120 HEFDADLOE--YFNAVLINE-RDKDGNFLGLK-----EFLIAPDNHFNLPNIS 168
Db 148 HRKQDNIKEEDIVYDAKDAELDDPESEDEVEGSASTLRIDIEDPN--FKN-KVNS 204
Oy 169 LSDVQVPTMYNKPALIVGVVYSLNKFVYDNPDRPSLIWQYFGSAKGFROYPGIK 228
Db 205 YAAVQIPTDIYKGSVTILNMLNWTALENVEMENRRQDPTLLQVGSATGVRYYPAPR 264
Oy 229 WEDENGVAFPCRNKNTYQAATSCKDYVILVYVSGSKGLRLTAKQTVSSILDTLD 288
Db 265 WRAPK-IDLYVRRRPVYIQGASSPKDYVILVYVSGSKGLRLTAKQTVSSILDTLD 323
Oy 289 DPEFNIAVNEELHYEPCINGTLYOADRKNKEHREHLDKLPAGKIGMIDLINAEFNI 348
Db 324 DDVYNVASENEKAQPVY-CFT-HLVQANRNKVFEEAOGMAKKTGTGKAEFAFDQ 381
Oy 349 LSDFNHTGGGSGISQAIMLITDGAVDYDTITFAKYNMPDKRYLITYLIGREAFADNK 408
Db 382 LQNSNITRAN--CNKIMMFTDGEDRDVDVEKYNMPPRTVTFEFGQINIDVTPIQ 439
Oy 409 WMACANKGEFTQISTLADVOENMEYLHLSRPKYI--DOEHVYVTEAYIDSTLTDDG 466
Db 440 WMACANKGYEPEIPISGIRINTOEYLDVGRPMVLAGEAKQVOMTNYEDAL-----G 494
Oy 467 PYLMTVAMPVES-----KONETRSKGILLGVGTDVPVKELTKTPKXKLGICGYA 518
Db 495 LGLVVTGTLPEVFNLTQDGEKKNO-----LILGVMGIDVALNDIKRLTPNTTLGANGV 549
Oy 519 FAITNNGYILTHPELRLLYEEGKRRKPNYSVSDSEVEMEDRDVLFNANMNRKTGKS 578
Db 550 FAIDNGVYLHLPNK-----POTTNPREVYTDLPDALEDEKEETIRSMIDONKCHKQI 606
Oy 579 MEVKTVDKGRKVLVMTNDYYTIDIGTPFSLGVALSRGKGKFFRGVNTIEGGLDLEH 638
Db 607 RTLYVSLDE--RYIDEVTRNTVWPIRSTNYSGLVLP--PYSTFYLOANLSDQILQVKLRI 662
Oy 639 PDVSLADEN-----SYCNTDLHPEHRLSLE-AIKLYLKGKEPLQOCDEKLEIO 686
Db 663 FEFLRSSFESEGHVFIAPREYCK-DLNASDNNTEFLKMFILMEKVTDPDSKCNFLH 721
Oy 687 EYLED-AVVSADIEAYWTSLALNKSSENSDKGEVAFIAGRTGLSRINLFGVAGQLTNODP 745
Db 722 NLIDTGITOQLVERVMRQODLN-----TYSLLAVFAATDGTITRVFPNKAEDMT----- 772
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OY 746 LKAGDKNIFNADHFPPLVYRAAEIOIPGSFYVSIPEFTG---PVNKS---VVTASTSIQ 799
DB 773 -----ENPEFPNAs-----FYRSLDN--HGYYFKPPHODALLRPLELNDYGIIVSTAVE 822
OY 800 LLDERSKSPVAAVGIOMLKEFFQKFWTAS-----ROCASLDGCSISCD--DETV 848
DB 823 LSLGRRTLRPAVVGKLDLEMAAEKFKVLASNRTHODOPKCGP--NSHCMDCEVNNBDL 881
OY 849 NCYLIDNNGFTLVs---EDYTQTDGFECEIGAVANNKLLTMSGSKRITLYVOAMCRANK 905
DB 882 LCVLIDOGFLVLSNQHOMQOVGRFSEVDANLMLALYNSFYTRKESYDYOAAACAP 941
OY 906 ESSGCA--HGLDPPYNA-----FLSAVKIMTELVLFLVEFNICSMWSDMTAKAOKL 956
DB 942 PGNIAGAPRGVFPVADFLNLAMWTSAAMSLFCOLLGLIYH--SWFOAD-PAEAEGS 998
OY 957 KOTLEPCOTEPAPVSEKTKET-----TGNACEDCSFVYIQOIPSNLNV 1005
DB 999 PETRE-----SSCYMKOTOTYFGSVASNAATIDCGNSCLFHAQRLTNLTLFV 1048
OY 1006 VVDSCLCESVAPITMAPETIRYNESLKERLKAOKIRRPESCHGFPEENARECG-CA 1064
DB 1049 VAEKP-LCSOGEAGRLLOKEHNSDGPBECGLVORPRYRGPHICDYATEDTSDCGKA 1107
OY 1065 PSLQAOYVLLPLLLML 1082
DB 1108 SFPPSLGLVLSLOLLLL 1125

RESULT 11
OY9268 PRELIMINARY: PRT: 1145 AA.
AC Q9Y268;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)
DE KIA0558 PROTEIN.
GN KIA0558.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRNIN;
RA Sekido Y., Duh F.-M., Latif F., Ding J., Lin J., Mathis M.,
Mauna J.D.;
RT "Gene 26, a new candidate human tumor suppressor gene located in the
3p21.3 small cell lung cancer homozygous deletion region homologous to
a voltage gated calcium channel alpha 2/ delta subunit."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Wei M.-H., Latif F., Duh F.-M., Adreazoli-Angeloni D., Kaashaba V.,
Zabarovskiy E., Johnson B., Lerman M.I.;
RT "A new alpha 2 delta subunit of the L-type voltage gated calcium
channel resides in the lung cancer critical region on 3p21.3."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=BRNIN;
RA MEDLINE=98290545; PubMed=9628581;
RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. IX.
The complete sequences of 100 new cDNA clones from brain which can
code for large proteins in vitro."
RL DNA Res. 5:31-39(1998).
DR EMBL: AF040709; AAC70914.1; -
DR EMBL: AF042792; AAB96913.1; -
DR EMBL: AB011130; BAA25484.1; -
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; VMA.

DR Pfam; PF02743; Cache: 1.
DR SMART; SM00327; VMA; 1.
DR PROSITE; PS0234; VMA; 1.
SQ SEQUENCE 1145 AA; 129268 MW; 9ADA4807FC70971B CRC64;
Query Match 21.2%; Score 1200; DB 4; Length 1145;
Best Local Similarity 29.7%; Pred. No. 2.4e-71;
Matches 345; Conservative 223; Mismatches 447; Indels 148; Gaps 43;
OY 3 GPGSRRAS---RGASALLAAALYALAGDVRSQQLPLSVYKIMAAAFGEIKSIKAK 59
DB 30 GGTGRRPTSGPPRLMLPLPLPLAAGASAYSPQ--QHTMGARRLEQVGVKRI 87
OY 60 YSGSGLQKKYKEYKDVAIEIDGLQVLKAKMEEMFHKSSAVRIVEAEALILK 119
DB 88 FCGVQQLREIKKDNRLNEVEQENEPQKLYEKVAGIESLDRKVALRLDAANPQKA 147
OY 120 HEFDADQYE--YFNAVLINL-RDKDGNFELK-----EFTLADNDFNNILPVNIS 168
DB 148 HRMDNKEEDIVYYDAKADAEIDPDESEDEYRGSKASTLRIDFEDBN--FKN-KVNS 204
OY 169 LSDVQVPTNNMKDPAIYNGVYMSLKKVYVNDNRDPSLIMQVFGSAKGFRRYPCIK 228
DB 205 YAAVOIPPTDIYKGVTLINLNMWTEALENEMENRRDPTLLMOVGSATGVTRYPATP 264
OY 229 WEPDENGVAIEDCRNRKRYIOAATSPKDVILVDSGSMKGLRLTIKQTVSSIIDTGD 288
DB 265 WRAPKK-IDLYDVRRRPYIGCASSPKDMVITVDVSGSVGLTLKMTKTSVCEMLDITSD 323
OY 289 DDFENIILAYNEBLAYVEPCLNGTLVQADRTNKEHREHLKILFAKGIGMLDIALNEAFNI 348
DB 324 DDYVNVASFNEKAQPVs-CFT-HLVQANVRNKKYKFEKVAQVAKTGYKAGFEYADQ 381
OY 349 LSDENHTQGSICSAQIMLIDTIDTIFAKNMPDNRVRIETVYLGREAPRADULK 408
DB 382 LQNSNITRAN--CNKIMMFIDGGEVDQVDFEKNMPEKRYRVEFVSQGNNDVDTPLQ 439
OY 409 WMAANKGFPTQISTLADQENVMELVLSRPKYI--DOEHDVYVTEAYIDSTLTDDOG 466
DB 440 WMAANKKYFEIPEISGIRINTQGLYDLVGRPNVLAKKAKQYQMTVYEDAL-----G 494
OY 467 PVLMTTVAMPVS-----KQNETRSKGILLGVGTDVPYKELKTIPIKKKIGIHGA 518
DB 495 LGLVVTGTPFLPFNLQDQDPGRKKNQ----LILGWDIVDALNDIKRLTPNTLTKANQYV 549
OY 519 FAITNNGYILHRELRLILYEEGKKRRKRKNYSVDLSEVEMDRODVILNANVRKTKFS 578
DB 550 FAIDLNGVLLHPNLK--POTTNFERPVTLDFDLDALEDEKKEIRKSMIDGNKHQOI 606
OY 579 MEVKTVYKGRVLMVMTNDYYTIDIKGTFPSLGVALSNGHKYFPRGAVTIEGLHLEH 638
DB 607 RTLVKSLDE-RYIDEVTNTYTWVPIRSTNYSGLVLP-PYSGFYIQAN--LSDQTLQYK 662
OY 639 PDVSLADEW-----SYCNTDLHPEHRHLSQLE-AIKLYLKGEPLLOCKELIQ 686
DB 663 FEFLIPSSFESEGHFIAPREYCK-DLNASDNTEFLKNEFLTELMKVPYPSDKQCNFFLH 721
OY 687 EYVLD-AVYSAPIEAVYSLALNKSSENDSKQVEVAFLOTGRGLSINLFPVGAEOITNDF 745
DB 722 NLIDLTGITQOLVERVWMDQDLN---TYSLLAVFAATDGTIRVFPNKAEDMT---- 772
OY 746 LKAGDKNIFNADHFPPLVYRAAEIOIPGSFYVSIPEFTG---PVNKS---VVTASTSIQ 799
DB 773 -----ENPEFPNAs-----FYRSLDN--HGYYFKPPHODALLRPLELNDYGIIVSTAVE 822
OY 800 LLDERSKSPVAAVGIOMLKEFFQKFWTAS-----ROCASLDGCSISCD--DETV 848
DB 823 LSLGRRTLRPAVVGKLDLEMAAEKFKVLASNRTHODOPKCGP--NSHCMDCEVNNBDL 881
OY 849 NCYLIDNNGFTLVs---EDYTQTDGFECEIGAVANNKLLTMSGSKRITLYVOAMCRANK 905
DB 882 LCVLIDOGFLVLSNQHOMQOVGRFSEVDANLMLALYNSFYTRKESYDYOAAACAP 941

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OY 906 ESSDGA--HGILDPYNA-----FLSAVKMIMTELVLFLVEFNLCSSWMSHDMTAKOQL 956
DB 942 PGNLAABRGVFPVPAVDFNLAMWTSAAMSLEFOOLLGLYLH--SWQAD-PARAECS 998
OY 957 KOTLEPCDTEVPAYFSERTIKET-----TGNINACEDCSKSFVIOQIPSSNLFVW 1005
DB 999 PETRE-----SSCMKOTQYYPFGSVNAYNAIIDCGSCRFHQRRLTNLLEFV 1048
OY 1006 VVDSCL--CES---VADITMAPIEIRNESLKERLKAQKIRRPES-CHGFHPEENARE 1060
DB 1049 VAEKPLSCQCEAGRLLQKETHCPAD---GPEQCELYORPRYRRGPHICFDYNATEDSD 1104
OY 1061 CG-GAPSLQAQTVLLPLLLML 1082
DB 1105 CGRGASPPPSLGLVLSQLLLLL 1127

RESULT 12
O9UEW0 PRELIMINARY; PRT; 1076 AA.
AC O9UEW0:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE ALPHA 2 DELTA CALCIUM CHANNEL SUBUNIT ISOFORM II.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wei M.-H., Latif F., Duh F.-M., Adreazoli-Angeloni D., Kashuba V.,
RA Zadorovskiy E., Johnson B., Lerman M.I.;
RA "A new alpha 2 delta subunit of the L-type voltage gated calcium
RT channel resides in the lung cancer critical region on 3p21.3.";
RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF042793; AAB96914.1; -
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; vMFA.
DR Pfam: PF02743; Cache; 1.
DR SMART: SM00327; vMA; 1.
DR PROSITE: PS50234; vMFA; 1.
SQ SEQUENCE 1076 AA; 122116 MW; EEC474836B7EDA85 CRC64;
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OY 394 TYLIGREAAEADNLKMKACANKGFPTQISTLADVOENMEXLVLSPKVY--DQEHNV 451
DB 356 TFSVGGHNTVDVPLQWMAACNKGYFEIPSIGAIRINTQYDVLVGLGPRVLAKREAKOYO 415
OY 452 WTEAVYIDSTLTDGQVPLMTVMAMPVS-----KONETRSKGLLGVGTQDVPEKL 503
DB 416 WTVNYEDAL-----GLGLVYTGTLFVFNLTQDQDGERKNG-----LLTGWGLDVALNL 465
OY 504 LKTIPIYKILGHCYAPATNGYIILTHPELRLLYEGRKRRKPNYSVDLSEVEMEDRD 563
DB 466 KRLTPVYTLGANGYVAIDNGYVLLHPNLK---PQTNREPVTLDLFAELEDENKEE 522
OY 564 VLPNMAVNRKTKFSMEVKKTVDKGRVLMNTDYTYTDIKGPPSLGVALSHGKRYFE 623
DB 523 IRRSMIDGKNKGHRQIRTVLKSIDE-RYIDEVTNRYWPVIRSTNYSLGLVP--PYSTFYL 580
OY 624 RGNVTEEGHLHDEHPDVSLADEM-----SYCNTDLPEHRHLSOLE-AIKLYL 671
DB 581 QAN--LSQDILQYKFEFLLPSSFESEGHVFIAPREYCK-DNADSNNTPEFLKNFIEIME 637
OY 672 KGKEPLLQCDKELIQEVLVD-AVVSAPTEAYWTSIALNSENDSKGEVAFLCTPTGLSR 730
DB 638 KVPDPSKQCCNFFLNLILDTGITQOLVERWRDODLN---TSLIAFAFATDGGITR 692
OY 731 INFVGAEOULTNDQFLKAGDKENIFNADHPRLMYRRARAEOIPGSFYYSIFSTG---PVN 787
DB 693 VEPNKAAEWMT-----ENPEPFNAS---FYRSLDN--HGyVFKPPHQQALLRPLE 738
OY 788 KSN---VVTASTISQLDERKSPVVAVGOMKLEFFORKEFTWAS-----ROCASTL 835
DB 739 LENDTVGILVSTAVEISLGRRTLRPAVGVKLLDEMAEKFVLAISRTQDDPOKCGP- 797
OY 836 DGKCSISCD--DETVNCYLIDNNGFTLVS--EDYTQTDGFEGELIGAVNKKLLTMGSEK 890
DB 798 NSHCMDCEVNNEDLICVLIDGDFLYLSNQNHQMPQVGFSEVDANLMLALYNNSFYT 857
OY 891 RITLYDYOAMCRANKRESSDGA--HGILDPYNA-----FLSAVKMIMTELVLVEFNL 941
DB 858 RKESYDYOAAACAPDPGNIGADRGVFPVPAVDFNLAMWTSAAMSLEFOOLLGLYLH- 916
OY 942 CSMWMSHDMTAKAOKLKOTLEPCDTEVPAYFSERTIKET-----TGNINACEDCSK 990
DB 917 -SWFQAD-PARAECSPETRE-----SSCMKOTQYYPFGSVNAYNAIIDCGSCSR 964
OY 991 SFVYIQIPSSNLFVVDSSCL--CES---VADITMAPIEIRNESLKERLKAQKIRRR 1045
DB 965 LFAQRLTYTNLILFVAEKPLCSQCEAGRLLQKETHCPAD---GPEQCELYORPRYRRG 1020
OY 1046 PESCHGFHPEENARECG-GAPSLQAQTVLLPLLLML 1082
DB 1021 PHICFDYNATEDSDCGRGASPPPSLGLVLSQLLLLL 1058

RESULT 13
O9EOG2 PRELIMINARY; PRT; 1156 AA.
AC O9EOG2:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE VOLTAGE-DEPENDENT CALCIUM CHANNEL ALPHA-2-DELTA-2 SUBUNIT.
GN CACNA2D2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TKDU;
RX MEDLINE=21015416; PubMed=11130987;
RA Barclay J., Rees M.;
RT "Genomic organization of the mouse and human alphazdelta2 voltage-
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OC	Mammalia, Eutheria, Rodentia; Sciurognathi, Muridae; Murinae; Mus.
OC	NCBI_TaxId=10090;
OC	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=BRAIN;
RX	MEDLINE=97113514; PubMed=8955374;
RA	Angelotti T., Holmann F.;
RL	FEBS Lett. 397:331-337(1996).
CC	- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE
CC	- EXCITATION-CONTRACTION COUPLING.
CC	- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNIT
CC	- ALPHA-1, ALPHA-2, BETA AND GAMMA.
CC	- SUBUNIT: ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULFIDE
CC	LINKED.
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC	- ALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROTEIN, ISOFORMS 2A-2E
CC	ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE
CC	SEQUENCE SHOWN HERE IS THAT OF ISOFORM 2A.
CC	- TISSUE SPECIFICITY: ISOFORM 2A IS EXPRESSED IN SKELETAL MUSCLE
CC	AORTA, 2B IS EXPRESSED IN BRAIN, 2C IS EXPRESSED IN HEART, 2D I
CC	EXPRESSED IN HEART AND SMOOTH MUSCLE, AND 2E IS EXPRESSED IN
CC	SMOOTH MUSCLE. ALL FIVE ISOFORMS ARE EXPRESSED IN THE
CC	CARDIOVASCULAR SYSTEM.
CC	- PFM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED F
CC	A PRECURSOR FORM.
CC	- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.
DR	EMBL; U73484; AAB50139.1; -
DR	EMBL; U73485; AAB50140.1; -
DR	EMBL; U73483; AAB50138.1; -
DR	EMBL; U73486; AAB50141.1; -
DR	EMBL; U73487; AAB50142.1; -
DR	MGI; MGI:88295; Gacna2d1.
DR	InterPro: IPR004010; Cache.
DR	InterPro: IPR002035; VFMA.
DR	Pfam; PF02743; Cache; 1.
DR	Pfam; PF00092; vwa; 1.
DR	SMART; SM00327; VFMA; 1.
DR	PROSITE; PS50234; VFMA; 1.
KW	ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW	Calcium channel; Glycoprotein; Phosphorylation; Signal;
KW	Alternative splicing.
FT	SIGNAL 1 24
FT	CHAIN 25 957
FT	TRANSMEM 958 1103
FT	TRANSMEM 446 949
FT	TRANSMEM 918 942
FT	TRANSMEM 1079 1098
FT	MOD_RES 501 501
FT	MOD_RES 845 845
FT	CARBOHYD 92 92
FT	CARBOHYD 136 136
FT	CARBOHYD 184 184
FT	CARBOHYD 324 324
FT	CARBOHYD 348 348
FT	CARBOHYD 475 475
FT	CARBOHYD 604 604
FT	CARBOHYD 613 613
FT	CARBOHYD 625 625
FT	CARBOHYD 781 781
FT	CARBOHYD 824 824
FT	CARBOHYD 888 888
FT	CARBOHYD 895 895
FT	CARBOHYD 985 985
FT	CARBOHYD 998 998
FT	VARSPLIC 531 549
FT	VARSPLIC 531 554
FT	VARSPLIC 644 644
SO	SEQUENCE 1103 AA; 124629 MW; 103773B4735120D4 CRC64;
Query Match	20.6%; Score 1168.5; DB 11; Length 1103;
Best Local Similarity	28.7%; Pred. No. 2.9e-69;

CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN	(1)
OK	NCBI_TaxID=10090;
XN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE-BRAIN:
RX	MEDLINE=97113514; PubMed=8955374; Angelotti T., Hofmann F.; FEBS Lett. 337:331-337(1996).
RL	- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE EXCITATION-CONTRACTION COUPLING.
CC	- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS ALPHA-1, ALPHA-2, BETA AND GAMMA.
CC	- SUBUNIT: ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULFIDE LINKED.
CC	- SUDCELLULAR LOCATION: INTEGRAL MEMBRANE PROEIN.
CC	- ALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROIEIN, ISOFORMS 2A-2E ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN HERE IS THAT OF ISOFORM 2A. - TISSUE SPECIFICITY: ISOFORM 2A IS EXPRESSED IN SKELETAL MUSCLE AOTEA, 2B IS EXPRESSED IN BRAIN, 2C IS EXPRESSED IN HEART, 2D I EXPRESSED IN HEART AND SMOOTH MUSCLE, AND 2E IS EXPRESSED IN SMOOTH MUSCLE. ALL FIVE ISOFORMS ARE EXPRESSED IN THE CARDIOVASCULAR SYSTEM.
CC	- PFM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED F A PRECURSOR FORM.
CC	- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.
DR	EMBL; U73484; AAB50139.1; -
DR	EMBL; U73485; AAB50140.1; -
DR	EMBL; U73483; AAB50138.1; -
DR	EMBL; U73486; AAB50141.1; -
DR	EMBL; U73487; AAB50142.1; -
DR	MCD; MG1:88295; Cacaad21.
DR	InterPro: IPRO04010; Cache.
DR	InterPro: IPRO02035; WVFAs.
DR	Pfam; PF02743; Cache; 1.
DR	Pfam; PF00092; VWa; 1.
DR	SMART; SM00327; VWA; 1.
KW	PROSITE; PS50234; WVFAs; 1.
DZ	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW	Calcium channel; Glycoprotein; Phosphorylation; Signal;
KW	Alternative splicing.
FT SIGNAL	1..24 POTENTIAL.
FT CHAIN	25..957 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT
FT FT CHAIN	958..1103 L-TYPE CALCIUM CHANNEL DELTA SUBUNIT.
FT TRANSMEM	446..469 POTENTIAL.
FT TRANSMEM	918..942 POTENTIAL.
FT TRANSMEM	1079..1098 POTENTIAL.
FT MOD_RES	501..501 PHOSPHORYLATION (BY CAPK) (POTENTIAL.).
FT CARBOHYD	92..92 PHOSPHORYLATION (BY CAPK) (POTENTIAL.).
FT CARBOHYD	136..136 N-LINKED (GLCNAC...) (POTENTIAL.)
FT CARBOHYD	184..184 N-LINKED (GLCNAC...) (POTENTIAL.)
FT CARBOHYD	324..324 N-LINKED (GLCNAC...) (POTENTIAL.)
FT CARBOHYD	348..348 N-LINKED (GLCNAC...) (POTENTIAL.)
FT CARBOHYD	475..475 N-LINKED (GLCNAC...) (POTENTIAL.)
FT CARBOHYD	604..604 N-LINKED (GLCNAC...) (POTENTIAL.)
FT CARBOHYD	613..613 N-LINKED (GLCNAC...) (POTENTIAL.)
FT CARBOHYD	675..675 N-LINKED (GLCNAC...) (POTENTIAL.)
FT CARBOHYD	781..781 N-LINKED (GLCNAC...) (POTENTIAL.)
FT CARBOHYD	824..824 N-LINKED (GLCNAC...) (POTENTIAL.)
FT CARBOHYD	888..888 N-LINKED (GLCNAC...) (POTENTIAL.)
FT CARBOHYD	895..895 N-LINKED (GLCNAC...) (POTENTIAL.)
FT CARBOHYD	985..985 N-LINKED (GLCNAC...) (POTENTIAL.)
FT CARBOHYD	998..998 N-LINKED (GLCNAC...) (POTENTIAL.)
FT VARSPLIC	531..549 MISSING (IN ISOFORMS 2B AND 2D).
FT VARSPLIC	554..554 MISSING (IN ISOFORMS 2C AND 2E).
FT VARSPLIC	644..644 Y-> SKGKMMD (IN ISOFORMS 2A, 2D AND 2E).
SQ SEQUENCE	1103 AA; 124629 MW; 103773BA73512004 CRC64;
Query Match 20.6%; Score 1168.5; DB 11; Length 1103;	
Best Local Similarity 28.7% ; Pred. No. 2.9e-69;	

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